

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 3, 2006, 03:53:44 ; Search time 3506.39 Seconds
(without alignments)
3255.375 Million cell updates/sec

Title: US-10-635-908-6
Perfect score: 617
Sequence: 1 DVKLVSQGGVLKGGSLKLT.....RSGYFMDYGOQTSVTVES 119

Scoring table: HLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+
-Q=/abs/ABSSWEB.spool/US10635908/runat_02062006_104214_10235/app_query.fasta_1
-DB=GenEmbl -OPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcp -NORW=exr -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h
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-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*

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2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_scs:*
8: gb_sy:*
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10: gb_vl:*
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12: gb_hlg:*
13: gb_in:*
14: gb_cm:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	617	100.0	357	2 AX556872 Sequence
2	617	100.0	1056	2 AX363232 Sequence
3	617	100.0	1411	2 AX363234 Sequence

4	617	100.0	1702	2 AX363235	AX363235 Sequence
5	617	100.0	2431	2 AX614787	AX614787 Sequence
6	559	90.6	432	6 MMIGHV3B6	X91667 M.musculus
7	559	90.6	432	6 MMIGHV5A6	X91668 M.musculus
8	559	90.6	474	2 AR080862	AR080862 Sequence
9	559	90.6	474	2 AR080864	AR080864 Sequence
10	539	87.4	422	2 BD260215	BD260215 Somatic t
11	539	87.4	422	2 BD260216	BD260216 Somatic t
12	539	87.4	422	2 AX042383	AX042383 Sequence
13	539	87.4	422	2 AX042384	AX042384 Sequence
14	537.5	87.1	419	2 BD260217	BD260217 Somatic t
15	537.5	87.1	419	2 BD260218	BD260218 Somatic t
16	533.5	86.5	419	2 AX042386	AX042386 Sequence
17	533.5	86.5	419	2 AF052835	AF052835 Mus muscu
18	530.5	86.0	1671	6 AF052835	AF052835 Mus muscu
19	529.5	85.8	360	6 MUSIGH2PRA	M26986 Mus muscu
20	516.5	83.7	339	6 MMIGH62	Y00744 Mouse rear
21	514.5	83.4	342	6 MMIGH62	X65785 M.musculus
22	513	83.1	735	2 E13598	E13598 DNA encodin
23	512.5	83.1	360	6 MUSIGH3C2A	L30142 Mus muscu
24	511.5	82.9	360	6 AY674872	AY674872 Mus muscu
25	511.5	82.9	360	6 AY674873	AY674873 Mus muscu
26	511.5	82.9	360	6 MUSIGH3ESA	L31896 Mus muscu
27	511	82.8	363	2 E12951	E12951 DNA encodi
28	511	82.8	363	2 E13910	E13910 DNA encodin
29	510.5	82.7	501	6 MUSIGHV	L41626 Mus muscu
30	506	82.0	363	2 E13912	E13912 DNA encodin
31	505.5	81.9	360	6 MUS2H1VH	L05431 Mouse mRNA
32	502	81.4	354	2 E16083	E16083 cDNA encodi
33	500.5	81.1	366	2 BD174582	BD174582 Gene enco
34	500.5	81.1	366	6 AB079937	AB079937 Mus muscu
35	500.5	81.1	1671	6 AF052834	AF052834 Mus muscu
36	499	80.9	339	6 MUSIGC	I23152 Mus muscu
37	498	80.7	484	2 AR648819	AR648819 Sequence
38	497.5	80.6	360	6 MMU309276	AJ309276 Mus muscu
39	495.5	80.3	354	6 MDIGMVB	Z22132 M.domeesticu
40	494.5	80.1	669	6 MMU62650	U62650 Mus muscu
41	494	80.1	363	6 AF178589	AF178589 Mus muscu
42	493	79.9	354	6 MMVHMRB2	X63788 M.musculus
43	492.5	79.8	354	6 AY648638	AY648638 Mus muscu
44	491	79.6	369	6 MMU277218	AJ277218 Mus muscu
45	490	79.4	369	6 MMU277220	AJ277220 Mus muscu

ALIGNMENTS

RESULT 1
AX556872
LOCUS AX556872 357 bp DNA
DEFINITION Sequence 1 from Patent WO02062972.
ACCESSION AX556872
VERSION AX556872.1 GI:25899970

SOURCE
ORGANISM
synthetic construct
other sequences: artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
Oosterwijk, E., Warnaar, S. and Ullrich, S.
Hybridoma cell line g250 and its use for producing monoclonal
antibodies
Patent: WO 02062972-A 1 15-AUG-2002;
Wiley AG (DE)

FEATURES
source
location/Qualifiers
1..357
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="mouse/human chimeric antibody gene"

ORIGIN

Alignment Scores:
Pred. No.: 3,896-67 Length: 357
Score: 617.00 Matches: 119

Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 2
Conservative: 0
Matches: 0
Indels: 0
Gaps: 0

US-10-635-908-6 (1-119) x AX556872 (1-357)

QY 1 AapVallyLeuValIGlUSeRgLyGlyLeuVallyLeuGlyGlySerLeuLyLeu 20
DB 1 GACGTGAAGCTGCTGAGTCTGGGGAGGCTTAGAGAGCTTGAGAGGCTCCCTGAAACCTC 60
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrrTyrMetSerTrpValArgGlnThr 40
DB 61 TCCTGTGACGCTCTGAGATTCACTTCACTAATTAATGATGATGATGATGATGATGATGATGAT 120
QY 41 ProGluLyArgLeuGluLeuValAlaAlaAlaLeuSerAspGlyGlyLeuThrTyrrTyr 60
DB 121 CCAGAGAAGAGGCTGGAGTGGTCCGACCATTAATAGATGATGATGATGATGATGATGATGAT 180
QY 61 LeuAspThrVallyGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrr 80
DB 181 CTAGACACGTGAAGGCGGATTCACCATTTCAAGAGACAAATGCCAAGAACCCCTGTAC 240
QY 81 LeuGlnMetSerSerLeuLySerGlyuAspThrAlaLeuPheTyrrCyAlaArgHisArg 100
DB 241 CTGCAGAAATGACAGCTGAGTCTGAGCTGAGACACAGCCTTTTACTGTGCAAGACACCC 300
QY 101 SerGlyTyrrPheSerMetAspTyrrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 301 TCGGGCTACTTTTCTATGACTACTGCGGCTCAAGGAACCTCAGTCACCGTCTCTCA 357

RESULT 2
AX363232
LOCUS AX363232 1056 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 8 from Patent WO0208263.
ACCESSION AX363232
VERSION AX363232.1 GI:18695369

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Lindholm, L., Nord, A. K. and Boulanger, P. A.
Modified virus having an altered tropism
Patent: WO 0208263-A 8 31-JAN-2002;
GOT-A- GENE AB (SE)

FEATURES
source
1. 1056
Location/Qualifiers

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="G250 construct"

ORIGIN

Alignment Scores:

Pred. No.: 1.19e-66 Length: 1056
Score: 617.00 Matches: 119
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-6 (1-119) x AX363232 (1-1056)

QY 1 AapVallyLeuValIGlUSeRgLyGlyLeuVallyLeuGlyGlySerLeuLyLeu 20
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QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrrTyrMetSerTrpValArgGlnThr 40
DB 436 TCCTGTGACGCTCTGAGATTCACTTCACTAATTAATGATGATGATGATGATGATGATGATGAT 495
QY 41 ProGluLyArgLeuGluLeuValAlaAlaAlaLeuSerAspGlyGlyLeuThrTyrrTyr 60

DB 496 CCAGAGAAGGCTGAGATTGCTCCGACCATTAATGATGATGATGATGATGATGATGATGATGAT 555
QY 61 LeuAspThrVallyGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrr 80
DB 556 CTAGACACGTGAAGGCGGATTCACCATTTCAAGAGCAATGCCAAGAACCCCTGTAC 615

QY 81 LeuGlnMetSerSerLeuLySerGlyuAspThrAlaLeuPheTyrrCyAlaArgHisArg 100
DB 616 CTGCAGAAATGACAGCTGAGTCTGAGCTGAGACACAGCCTTTTACTGTGCAAGACACCC 675
QY 101 SerGlyTyrrPheSerMetAspTyrrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 676 TCGGGCTACTTTTCTATGACTACTGCGGCTCAAGGAACCTCAGTCACCGTCTCTCA 732

RESULT 3
AX363234
LOCUS AX363234 1411 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 10 from Patent WO0208263.
ACCESSION AX363234
VERSION AX363234.1 GI:18695371

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Lindholm, L., Nord, A. K. and Boulanger, P. A.
Modified virus having an altered tropism
Patent: WO 0208263-A 10 31-JAN-2002;
GOT-A- GENE AB (SE)

FEATURES
source
1. 1411
Location/Qualifiers

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Fiber construct A1 G250"

ORIGIN

Alignment Scores:
Pred. No.: 1.61e-66 Length: 1411
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-6 (1-119) x AX363234 (1-1411)

QY 1 AapVallyLeuValIGlUSeRgLyGlyLeuVallyLeuGlyGlySerLeuLyLeu 20
DB 722 GACGTGAAGCTGCTGAGTCTGGGGAGGCTTAGAGAGCTTGAGAGGCTCCCTGAAACCTC 781
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrrTyrMetSerTrpValArgGlnThr 40
DB 782 TCCTGTGACGCTCTGAGATTCACTTCACTAATTAATGATGATGATGATGATGATGATGATGAT 841
QY 41 ProGluLyArgLeuGluLeuValAlaAlaAlaLeuSerAspGlyGlyLeuThrTyrrTyr 60
DB 842 CCAGAGAAGGCTGAGTGGTCCGACCATTAATAGATGATGATGATGATGATGATGATGATGAT 901
QY 61 LeuAspThrVallyGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrr 80
DB 902 CTAGACACGTGAAGGCGGATTCACCATTTCAAGAGCAATGCCAAGAACCCCTGTAC 961
QY 81 LeuGlnMetSerSerLeuLySerGlyuAspThrAlaLeuPheTyrrCyAlaArgHisArg 100
DB 962 CTGCAGAAATGACAGCTGAGTCTGAGCTGAGACACAGCCTTTTACTGTGCAAGACACCC 1021
QY 101 SerGlyTyrrPheSerMetAspTyrrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 1022 TCGGGCTACTTTTCTATGACTACTGCGGCTCAAGGAACCTCAGTCACCGTCTCTCA 1078
RESULT 4

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

ORIGIN

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Pred. No.:      2,81e-66      Length:      2431
Score:          617.00      Matches:      119
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:      100.0%      Indels:      0
DB:                2      Gaps:      0

US-10-635-908-6 (1-119) x AK614787 (1-2431)

QY      1      AspValLysLeuValGluSerGlyGlyGlyLeuValLysLeuGlySerLeuLysLeu: 20
Db      843      GAGCTGAAGGCTCGTGAGTCTGGGGGAGGCTTAGTGAAGCTTGAGGAGGCTCCGTAACCTC
QY      21      SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTyrPValArgGlnThr 40
Db      903      TCGTGTGAGGCTCTGATTCACCTTCAAGTAACATTAACTGTTGGGTGGCAACT 962
QY      41      ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
Db      963      CCAAGAGAGAGGCTGGAGGTGGTGGACGCCATTAAITGATGTGTGATCACTACTAT 1022
QY      61      LeuAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
Db      1023      CTAGACACTGTGAAGGGCCCATTCACCATTTCAAGAGACATGCCAAGAACACCCCTGAC 1082
QY      81      LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
Db      1083      CTGCAAAATGAGACACTGGAAGTCTGAGAGACACACCTGTGTTTACTGTGCAAGACACGC 1142
QY      101      SerGlyTyrPheSerMetAspTyrTyrGlyGlnIleThrSerValThrValSerSer 119
Db      1143      TCGGCTACTTTCATGACTACTCTGGGGGTCAAGAACTCAGTCACCGTCTCTCA 1199

RESULT 6
M1GHV3B6      432 bp      mRNA      linear      ROD 24-OCT-1995
LOCUS      M1GHV3B6      432 bp      mRNA      linear      ROD 24-OCT-1995
DEFINITION      M.musculus mRNA for Ig heavy chain variable region (cell line 3B6).
ACCESSION      X91667
VERSION      X91667.1 GI:1001880
KEYWORDS      complementarity determining region; heavy chain; immunoglobulin
               variable region.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE      1
AUTHORS      Carceller, A., Rosell-Vives, E., Gomez-Roig, A., Adan, J., Sproll, M.
               and Philats, J.
TITLE      Immunological and structural properties of anti-idiotypic
               antibodies mimicking an epitope of human epidermal growth factor
               receptor
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 432)
AUTHORS      Rosell-Vives, E.
TITLE      Direct Submission
JOURNAL      Submitted (19-SEP-1995) E. Rosell-Vives, MERCK, Farma y Quimica
               S.A., Caspe 108, E-08010 Barcelona, SPAIN
FEATURES
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             /db_xref="taxon:10090"
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/cell_type="fusion of splenocytes x H1i friendly myeloma
653"
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/protein_id="CA62854.1"
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1..432
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148..162
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misc_feature
205..255
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misc_feature
352..399
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ORIGIN
Alignment Scores:
Pred. No.: 7.65e-60 Length: 432
Score: 559.00 Matches: 111
Percent Similarity: 92.8% Conservative: 5
Best Local Similarity: 88.8% Mismatches: 3
Query Match: 90.6% Indels: 6
DB: 6 Gaps: 2

US-10-635-908-6 (1-119) x MMIGHV3B6 (1-432)
QY 1 AapValIyLeuValIguSerIygiYgIyLeuValIyLeuGlyYgIySerIyLeu 20
Db 58 GAGGTGAAGCTCTGTGAAGTCTGGGGAGGCTTGTGAAGCTTGGAGGCTCCCGAAGCTC 117
QY 21 SerCyAlAlAlSerIyPheThrPheSerAsnTyTyMeSerTrpValArgGlnThr 40
Db 118 TCCTGTGACGCGCTCGATTCACTTCAGTAATTAATCACTTGGGTTGCCAGACT 177
QY 41 ProGluValArgLeuGluLeuValAlAlAlIeAsnSerAspGlyIyIleThrTyTy 60
Db 178 CCAGAGAAAGAGGTGGAGTTTGTGCGAGCCATTAAATGTAATGTGTGTGCACTACTAT 237
QY 61 LeuAspThrValIyLeuGlyArgPheThrIleSerArgAspAsnAlAlAsnThrLeuTy 80
Db 238 CCAGACACTGTGAAGGCGCGATTCACTCCAGAGACAAATCCAGAAACACCTGTAC 297
QY 81 LeuGlnMetSerSerLeuIySerIySerIyAspThrAlAlIeAsnPheTyCyAlAlArgH1sArg 100
Db 298 CTGCATATGAGAGCTGTGAAGTCTGAGACACAGCCCTTGATTAATCTGTGCAAGACATCGG 357
QY 101 -----SerIyTy-----PheSerMetAspTyTrpGlyGlnGlyThrSer 114
Db 358 GGGAGGAGACAGCTCGGGCTTACGTAAGGTATGCTATGACTACTGAGGCTCAAGGAACCTCA 417
QY 115 ValThrValSerSer 119
Db 418 GTCAACCTCTCTCA 432

RESULT 7
LOCUS MMIGHV5A6 432 bp mRNA linear ROD 24-OCT-1995
DEFINITION M.musculus mRNA for Ig heavy chain variable region (cell line 5A6).
ACCESSION X91668
VERSION X91668.1 GI:1001881
KEYWORDS complementarity determining region; heavy chain; immunoglobulin
variable region.
SOURCE Mus musculus (house mouse)

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Carceller,A., Rosell-Vives,E., Gomez-Rold,A., Adan,J., Sproll,M.
1 and Plutelsky,J.
TITLE Immunological and structural properties of anti-idiotypic
antibodies mimicking an epitope of human epidermal growth factor
receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 432)
AUTHORS Rosell-Vives,E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-1995) E. Rosell-Vives, MERCK, Farma y Quimica
S.A., Caspe 108, E-08010 Barcelona, SPAIN
FEATURES
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/strain="BALB/c"
/sub_strain="by J Ico"
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/chromosome="12"
/cell_line="5A6"
/cell_type="fusion of splenocytes x H1i friendly myeloma
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/issue_type="hybridoma"
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/product="immunoglobulin heavy chain"
/protein_id="CA62854.1"
/db_xref="GI:1008126"
/translation="MDSRLNLFVLVLKGVLCVRLVESGGGLVKGSLKSCAAS
GFTFSNYMSWRQTPKRLFEVAALNSGSGTTPDYKGFTRSDNAKNTLYLQM
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1..57
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1..432
/product="variable region of Ig heavy chain"
V_region
148..162
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/feature="complementarity-determining region 1"
misc_feature
205..255
/product="CDR2"
/feature="complementarity-determining region 2"
misc_feature
352..399
/product="CDR3"
/feature="complementarity-determining region 3"

ORIGIN
Alignment Scores:
Pred. No.: 7.65e-60 Length: 432
Score: 559.00 Matches: 111
Percent Similarity: 92.8% Conservative: 5
Best Local Similarity: 88.8% Mismatches: 3
Query Match: 90.6% Indels: 6
DB: 6 Gaps: 2

US-10-635-908-6 (1-119) x MMIGHV5A6 (1-432)
QY 1 AapValIyLeuValIguSerIygiYgIyLeuValIyLeuGlyYgIySerIyLeu 20
Db 58 GAGGTGAAGCTCTGTGAAGTCTGGGGAGGCTTGTGAAGCTTGGAGGCTCCCGAAGCTC 117
QY 21 SerCyAlAlAlSerIyPheThrPheSerAsnTyTyMeSerTrpValArgGlnThr 40
Db 118 TCCTGTGACGCGCTCGATTCACTTCAGTAATTAATCACTTGGGTTGCCAGACT 177
QY 41 ProGluValArgLeuGluLeuValAlAlAlIeAsnSerAspGlyIyIleThrTyTy 60
Db 178 CCAGAGAAAGAGGTGGAGTTTGTGCGAGCCATTAAATGTAATGTGTGTGCACTACTAT 237
QY 61 LeuAspThrValIyLeuGlyArgPheThrIleSerArgAspAsnAlAlAsnThrLeuTy 80

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Db 238 CCAGACACTGTGAAGGCGCATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 297
Qy 81 LeuGImeSerSerleuLysSerGluAspThrAlaLeuPheTyrCySaIaArgHisArg 100
Db 298 CTGCAGAAATGAGCAGTCTGAGTCTGAGGACACAGCCCTTGATTAATCTGTGCAAGACATCGG 357
Qy 101 -----SerGlyTyr-----PheSerMetAspTyrTrpGlyGlnGlyThrSer 114
Db 358 GGGAGGAGACAGCTCGGGCTACGAGGATATGCTATGACTACTAGGGGTCAAGGAACCTCA 417
Qy 115 ValThrValSerSer 119
Db 418 GTCAACCGTCTCTCA 432

RESULT 8
AR080862
LOCUS AR080862 474 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 5 from patent US 5969107.
ACCESSION AR080862
VERSION AR080862.1 GI:10007591
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 474)
AUTHORS Carceller,A., Rosell,E., Gomez,A., Adan,J. and Pinalts,J.
TITLE Anti-idiotypic antibodies which induce an immune response against
epidermal growth factor receptor
JOURNAL Patent: US 5969107-A 5 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..474
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 8,42e-60 Length: 474
Score: 559.00 Matches: 111
Percent Similarity: 92.8% Conservative: 5
Best Local Similarity: 88.8% Mismatches: 3
Query Match: 90.6% Indels: 6
DB: Gaps: 2

US-10-635-908-6 (1-119) x AR080862 (1-474)
Qy 1 AspValIlyLeuValGluSerGlyGlyLeuValIlyLeuGlySerLeuLysLeu 20
Db 58 GACGTGAAGCTCGTGAAGCTGGGGAGGAGCTTAGTGAAGCTGGAGGCTCCCGAAACTA 117
Qy 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgInThr 40
Db 118 TCCTGTGACGCTCTGATTCACCTTCAGTACTATTAACATGCTTGGGTTCCCAACT 177
Qy 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60
Db 178 CCAGAGAAAGAGCTGAGTCTGCGCAGCCATTATATGATGATGTTGTTACACTATAT 237
Qy 61 LeuAspThrValIlysgIyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
Db 238 CCAGACACTGTGAAGGCGCATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 297
Qy 81 LeuGImeSerSerleuLysSerGluAspThrAlaLeuPheTyrCySaIaArgHisArg 100
Db 298 CTGCAGAAATGAGCAGTCTGAGTCTGAGGACACAGCCCTTGATTAATCTGTGCAAGACATCGG 357
Qy 101 -----SerGlyTyr-----PheSerMetAspTyrTrpGlyGlnGlyThrSer 114
Db 358 GGGAGGAGACAGCTCGGGCTACGAGGATATGCTATGACTACTAGGGGTCAAGGAACCTCA 417
Qy 115 ValThrValSerSer 119
Db 418 GTCAACCGTCTCTCA 432

RESULT 9
AR080864
LOCUS AR080864 474 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 9 from patent US 5969107.
ACCESSION AR080864
VERSION AR080864.1 GI:10007593
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 474)
AUTHORS Carceller,A., Rosell,E., Gomez,A., Adan,J. and Pinalts,J.
TITLE Anti-idiotypic antibodies which induce an immune response against
epidermal growth factor receptor
JOURNAL Patent: US 5969107-A 9 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..474
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 8,42e-60 Length: 474
Score: 559.00 Matches: 111
Percent Similarity: 92.8% Conservative: 5
Best Local Similarity: 88.8% Mismatches: 3
Query Match: 90.6% Indels: 6
DB: Gaps: 2

US-10-635-908-6 (1-119) x AR080864 (1-474)
Qy 1 AspValIlyLeuValGluSerGlyGlyLeuValIlyLeuGlySerLeuLysLeu 20
Db 58 GACGTGAAGCTCGTGAAGCTGGGGAGGAGCTTAGTGAAGCTGGAGGCTCCCGAAACTC 117
Qy 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgInThr 40
Db 118 TCCTGTGACGCTCTGATTCACCTTCAGTACTATTAACATGCTTGGGTTCCCAACT 177
Qy 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60
Db 178 CCAGAGAAAGAGCTGAGTCTGCGCAGCCATTATATGATGATGTTGTTACACTATAT 237
Qy 61 LeuAspThrValIlysgIyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
Db 238 CCAGACACTGTGAAGGCGCATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 297
Qy 81 LeuGImeSerSerleuLysSerGluAspThrAlaLeuPheTyrCySaIaArgHisArg 100
Db 298 CTGCAGAAATGAGCAGTCTGAGTCTGAGGACACAGCCCTTGATTAATCTGTGCAAGACATCGG 357
Qy 101 -----SerGlyTyr-----PheSerMetAspTyrTrpGlyGlnGlyThrSer 114
Db 358 GGGAGGAGACAGCTCGGGCTACGAGGATATGCTATGACTACTAGGGGTCAAGGAACCTCA 417
Qy 115 ValThrValSerSer 119
Db 418 GTCAACCGTCTCTCA 432

RESULT 10
BD260215
LOCUS BD260215 422 bp DNA linear PAT 17-JUL-2003
DEFINITION Somatic transgene immunization and related methods.
ACCESSION BD260215
VERSION BD260215.1 GI:33069985
KEYWORDS DP 2002542305-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 422)
AUTHORS Zanetti,M.
TITLE Somatic transgene immunization and related methods

JOURNAL Patent: JP 2002542305-A 4 10-DEC-2002;
MAURIZIO ZANETTI, EUROGEN HOLDING SA
COMMENT OS Artificial Sequence
PN JP 2002542305-A/4
PD 10-DEC-2002
PF 27-APR-2000 JP 2000613478
PR 27-APR-1999 US 09/300959
PI MAURIZIO ZANETTI
PC A61K48/00, A61K31/711, A61K35/76, A61K38/00, A61K38/22, A61K38/36,
A61K39/395,
A61K37/46,
A61P31/12, A61P37/04, C12N5/10, C12N15/09, A61K37/02, A61K37/24, PC
A61K37/46,
PC C12N15/00, C12N5/00
CC Description of Artificial Sequence: genomic VDJ region FH
Key Location/Qualifiers
FT source 1..422
FT /organism='Artificial Sequence'.
FEATURES
source 1..422
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Alignment Scores:
Pred. No.: 2,29e-57 Length: 422
Score: 539.00 Matches: 107
Percent Similarity: 91.6% Conservative: 2
Best Local Similarity: 89.9% Mismatches: 10
Query Match: 87.4% Indels: 0
Gaps: 0
DB: 2
US-10-635-908-6 (1-119) x BD260215 (1-422)
QY 1 Aapvallyleuvalgluserglyylglyleuvallyleuvallyserleuylsleu 20
DB 1 GACGTGAAGCTGTGAGCTGTGGGAGGCTTAGTAAGCTTGAGAGGCTCCGAAACTC 60
QY 21 SerCyAlAlaSerGlyPheThrPheSerAenTYrTYrMetSerTrpValArgGlnThr 40
DB 61 TCTGTGACGCTCTGGATTCACTTCAGTAGGTAATTAATGCTTGGGTTGCCAGACT 120
QY 41 ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyylleThrTYrTYr 60
DB 121 CCAGAGAAAGAGCTGAGAGTGTGCGAGCATTAAATGTAATGTGTGACACTACTAT 180
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTYr 80
DB 181 CCAGACACTGTGAAGGCGGATTCACTCCAGAGCAATGCCAAAAACACCTGTGAC 240
QY 81 LeuGlnMetSerSerleuLysSerGluAspThrAlaLeuPheTYrCYsAlaArgHisArg 100
DB 241 CTGCAATAGAGAGCTGAGAGCTGAGAGCAGACGCTTGATTAATCTGTCAGAGAAAGTGA 300
QY 101 SerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 301 CCTACTCTCATGATGATGAGTAACTGAGGCTCAAGAACTCAGTCACTGCTCTCTCA 357
RESULT 11
BD260216 422 bp DNA linear PAT 17-JUL-2003
LOCUS BD260216
DEFINITION Somatic transgene immunization and related methods.
ACCESSION BD260216
VERSION BD260216.1 GI:33069986
KEYWORDS JP 2002542305-A/5.
SOURCE JP 2002542305-A/5.
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 422)
AUTHORS Zanetti, M.
TITLES Somatic transgene immunization and related methods
JOURNAL Patent: JP 2002542305-A 5 10-DEC-2002;
MAURIZIO ZANETTI, EUROGEN HOLDING SA

COMMENT OS Artificial Sequence
PN JP 2002542305-A/5
PD 10-DEC-2002
PF 27-APR-2000 JP 2000613478
PR 27-APR-1999 US 09/300959
PI MAURIZIO ZANETTI
PC A61K48/00, A61K31/711, A61K35/76, A61K38/00, A61K38/22, A61K38/36,
A61K39/395,
A61K37/46,
A61P31/12, A61P37/04, C12N5/10, C12N15/09, A61K37/02, A61K37/24, PC
A61K37/46,
PC C12N15/00, C12N5/00
CC Description of Artificial Sequence: genomic VDJ region FH
Key Location/Qualifiers
FT source 1..422
FT /organism='Artificial Sequence'.
FEATURES
source 1..422
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Alignment Scores:
Pred. No.: 2,29e-57 Length: 422
Score: 539.00 Matches: 107
Percent Similarity: 91.6% Conservative: 2
Best Local Similarity: 89.9% Mismatches: 10
Query Match: 87.4% Indels: 0
Gaps: 0
DB: 2
US-10-635-908-6 (1-119) x BD260216 (1-422)
QY 1 Aapvallyleuvalgluserglyylglyleuvallyleuvallyserleuylsleu 20
DB 1 GACGTGAAGCTGTGAGCTGTGGGAGGCTTAGTAAGCTTGAGAGGCTCCGAAACTC 60
QY 21 SerCyAlAlaSerGlyPheThrPheSerAenTYrTYrMetSerTrpValArgGlnThr 40
DB 61 TCTGTGACGCTCTGGATTCACTTCAGTAGGTAATTAATGCTTGGGTTGCCAGACT 120
QY 41 ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyylleThrTYrTYr 60
DB 121 CCAGAGAAAGAGCTGAGAGTGTGCGAGCATTAAATGTAATGTGTGACACTACTAT 180
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTYr 80
DB 181 CCAGACACTGTGAAGGCGGATTCACTCCAGAGCAATGCCAAAAACACCTGTGAC 240
QY 81 LeuGlnMetSerSerleuLysSerGluAspThrAlaLeuPheTYrCYsAlaArgHisArg 100
DB 241 CTGCAATAGAGAGCTGAGAGCTGAGAGCAGACGCTTGATTAATCTGTCAGAGAAAGTGA 300
QY 101 SerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 301 CCTACTCTCATGATGATGAGTAACTGAGGCTCAAGAACTCAGTCACTGCTCTCTCA 357
RESULT 12
AX042383 422 bp DNA linear PAT 23-NOV-2000
LOCUS AX042383
DEFINITION Sequence 5 from Patent WO0064488.
ACCESSION AX042383
VERSION AX042383.1 GI:11341000
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Zanetti, M.
TITLES Somatic transgene immunization and related methods
JOURNAL Patent: WO 0064488-A 5 02-NOV-2000;
Zanetti, Maurizio (US)
FEATURES
source 1..422
Location/Qualifiers

ORGIN

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="genomic VDJ region"

Alignment Scores:

Pred. No.:	2,296-57	Length:	422
Score:	539.00	Matches:	107
Percent Similarity:	91.6%	Conservative:	2
Best Local Similarity:	89.9%	Mismatches:	10
Query Match:	87.4%	Indels:	0
DB:	2	Gaps:	0

US-10-635-908-6 (1-119) x AX042383 (1-422)

QY 1 AspVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuValLeu 20
1 GACGTGAAGCTGCTGAGTCTGGGGAGGCTTAGGAACTTGGAGGGTCCCGAAATC 60
DB 1
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40
61 TCTGTGCAGCCTCTGATTCACCTTCAGTAGGTAATTAATGCTTGGGTTCCCGAGACT 120
DB 61
QY 41 ProGluLySarGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
121 CCAGAGAAAGGCTGGAGTGGTGGCAGACCATTAATAGTAATGGTGGTACACCTACTAT 180
DB 121
QY 61 LeuAspThrVallyGlyArgPheThrIleSerArgAspAsnAlaIlyAsnThrLeuTYr 80
181 CCAGACACTGTGAAGGCCGATTCACCATCTCCAGAGACAAATCCAAAAACACCTGTAC 240
DB 181
QY 81 LeuGluMetSerSerLeuLySerGlyUaspThrAlaLeuPheTYrCysAlaArgHisArg 100
241 CTGCATAATGACGCTGAAAGTCTGAGACACAGCCTTGTAATTAATCTGTGCAAGAAAGCTA 300
DB 241
QY 101 SerGlyTYrPheSerMetAspTYrTYrGlyGlnGlyThrSerValThrValSerSer 119
301 CCTACTCTCATGTAATGACTACTGCGGTCAAGAAACCTCAAGTACCGTCTCTCA 357
DB 301

RESULT 13
AX042384 422 bp DNA linear PAT 23-NOV-2000
LOCUS
DEFINITION Sequence 6 from Patent WO0064488.
ACCESSION AX042384
VERSION AX042384.1 GI:11341001

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1
Zanetti, M.
Somatic transgene immunization and related methods
Patent: WO 0064488-A 6 02-NOV-2000;
Zanetti, Maurizio (US)
location/Qualifiers

FEATURES
source
1..422
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="genomic VDJ region"

ORIGIN

Alignment Scores:

Pred. No.:	2,296-57	Length:	422
Score:	539.00	Matches:	107
Percent Similarity:	91.6%	Conservative:	2
Best Local Similarity:	89.9%	Mismatches:	10
Query Match:	87.4%	Indels:	0
DB:	2	Gaps:	0

US-10-635-908-6 (1-119) x AX042384 (1-422)

QY 1 AspVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuValLeu 20
1 GACGTGAAGCTGCTGAGTCTGGGGAGGCTTAGGAACTTGGAGGGTCCCGAAATC 60
DB 1
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40
61 TCTGTGCAGCCTCTGATTCACCTTCAGTAGGTAATTAATGCTTGGGTTCCCGAGACT 120
DB 61
QY 41 ProGluLySarGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
121 CCAGAGAAAGGCTGGAGTGGTGGCAGACCATTAATAGTAATGGTGGTACACCTACTAT 180
DB 121
QY 61 LeuAspThrVallyGlyArgPheThrIleSerArgAspAsnAlaIlyAsnThrLeuTYr 80
181 CCAGACACTGTGAAGGCCGATTCACCATCTCCAGAGACAAATGCCAAAAACACCTGTAC 240
DB 181
QY 81 LeuGluMetSerSerLeuLySerGlyUaspThrAlaLeuPheTYrCysAlaArgHisArg 100
241 CTGCATAATGACGCTGAAAGTCTGAGACACAGCCTTGTAATTAATCTGTGCAAGAAAGCTA 300
DB 241
QY 101 SerGlyTYrPheSerMetAspTYrTYrGlyGlnGlyThrSerValThrValSerSer 119
301 CCTACTCTCATGTAATGACTACTGCGGTCAAGAAACCTCAAGTACCGTCTCTCA 357
DB 301

RESULT 14
BD260217 419 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Somatic transgene immunization and related methods.
ACCESSION BD260217
VERSION BD260217.1 GI:33069987
KEYWORDS JP 2002542305-A/6.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 419)
Zanetti, M.
Somatic transgene immunization and related methods
Patent: JP 2002542305-A 6 10-DEC-2002;
MAURIZIO ZANETTI, EUROGEN HOLDING SA
OS Artificial Sequence
PN JP 2002542305-A/6
PD 10-DEC-2002 JP 200613478
PF 27-APR-2000 JP 200613478
PR 27-APR-1999 US 09/300959
PI MAURIZIO ZANETTI
PC A61K48/00, A61K31/711, A61K35/76, A61K38/00, A61K38/22, A61K38/36,
PC A61K39/395,
PC A61P31/12, A61P37/04, C12N5/10, C12N5/09, A61K37/02, A61K37/24, PC
A61K37/46,
PC C12N15/00, C12N5/00
CC Description of Artificial Sequence: genomic VDJ region FH
Key Location/Qualifiers
FT source 1..419
/organism="Artificial Sequence".

FEATURES

source
1..419
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores:

Pred. No.:	3,496-57	Length:	419
Score:	537.50	Matches:	107
Percent Similarity:	92.4%	Conservative:	3
Best Local Similarity:	89.9%	Mismatches:	8
Query Match:	87.1%	Indels:	1
DB:	2	Gaps:	1

US-10-635-908-6 (1-119) x BD260217 (1-419)

QY 1 AspVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuValLeu 20
1 GACGTGAAGCTGCTGAGTCTGGGGAGGCTTAGGAACTTGGAGGGTCCCGAAATC 60
DB 1

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Db      1  GACGTGAAGCTGTGGAGCTTGGGGAGGCTTAGTGAAGCTTGGAGGGCTCCGTGAAGCTC 60
QY      21  SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40
Db      61  TCCTGTGACGCTCTGGATTCACTTTCAGTAGATTAATGATGCTTGGGTTGCCAGACT 120
QY      41  ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
Db      121  CCAGAGAAGAGGCTGAGTGGTCCAGCATTAATGAAATGGTGTAGACCTACATAT 180
QY      61  LeuAspThrValIleGlyValArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTyr 80
Db      181  CCAGACACTGTGAAGGGCCGATTCCACCATCTCCAGAGCAATGCCAAAACACCTGTAC 240
QY      241  CTGCAAAATGAGCAGTCTGAAGTCTGAGACACAGCCTGTATTAATTAATCTGTGCAAGAAAGCC 300
Db      301  TACTCTCAT---GGTATGAGCTACTGGGGTCAAGAACTCAGTCACCGTCTCTCA 354
QY      101  SerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 119
Db      301  TACTCTCAT---GGTATGAGCTACTGGGGTCAAGAACTCAGTCACCGTCTCTCA 354

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RESULT 15

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AX042385      419 bp      DNA      linear      PAT 23-NOV-2000
LOCUS      AX042385
DEFINITION      Sequence 7 from Patent WO0064488.
ACCESSION      AX042385
VERSION      AX042385.1  GI:11341002
KEYWORDS
SOURCE
ORGANISM      synthetic construct
              other sequences; artificial sequences.

```

```

REFERENCE
AUTHORS      Zanetti, M.
TITLE      Somatic transgene immunization and related methods
JOURNAL      Patent: WO 0064488-A 7 02-NOV-2000;
              Zanetti, Maurizio (US)
              location/Qualifiers

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FEATURES
source
1..419
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="genomic VDJ region"

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ORIGIN

Alignment Scores:

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Pred. No.:      3,49e-57      Length:      419
Score:          537.50      Matches:      107
Percent Similarity: 92.4%      Conservative: 3
Best Local Similarity: 89.9%      Mismatches: 8
Query Match:    87.1%      Indels:      1
DB:              Gaps:      1

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```

US-10-635-908-6 (1-119) x AX042385 (1-419)

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QY      1  AapValIleLeuValGluSerGlyGlyGlyLeuValIleLeuGlyGlySerLeuIleValLeu 20
Db      1  GACGTGAAGCTGTGGAGCTTGGGGAGGCTTAGTGAAGCTTGGAGGGCTCCGTGAAGCTC 60
QY      21  SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40
Db      61  TCCTGTGACGCTCTGGATTCACTTTCAGTAGATTAATGATGCTTGGGTTGCCAGACT 120
QY      41  ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
Db      121  CCAGAGAAGAGGCTGAGTGGTCCAGCATTAATGAAATGGTGTAGACCTACATAT 180
QY      61  LeuAspThrValIleGlyValArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTyr 80
Db      181  CCAGACACTGTGAAGGGCCGATTCCACCATCTCCAGAGCAATGCCAAAACACCTGTAC 240
QY      81  LeuGluMetSerSerLeuIleValSerGlyAspThrAlaLeuPheTyrCysAlaArgHisArg 100

```

```

Db      241  CTGCAAAATGAGCAGTCTGAAGTCTGAGACACAGCCTTGTATTACTGTGCAAGAAAGGCC 300

```

```

QY      101  SerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 119
Db      301  TACTCTCAT---GGTATGAGCTACTGGGGTCAAGAACTCAGTCACCGTCTCTCA 354

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Search completed: June 3, 2006, 06:56:33
Job time : 3509.39 secs

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XX 07-FEB-2001; 2001US-0266853P.
PR 05-OCT-2001; 2001US-0327008P.
XX (WILE-) WILEX AG.
XX Oosterwijk E, Wijnhaar S, Ulrich S;
XX WPI; 2002-627544/67.
DR P-PsDB; ABB79886.
XX
XX Novel hybridoma cell capable of producing monoclonal antibody G250, which
PT is useful in the treatment of renal cell carcinoma and metastases after
PT tumor surgery.
XX
XX Example 3; Fig 1; 20pp; English.
XX
XX The present sequence is the coding sequence for the heavy chain variable
CC region (VH) of murine monoclonal antibody (Mab) G250. The coding sequence
CC was obtained from a clone obtained by PCR amplification of hybridoma G250
CC (DSM ACC 2526) cDNA and cloning into vector pUC19. Mab G250 (IgG1)
CC recognises MN antigen, which is preferentially expressed on membranes of
CC renal cell carcinoma cells and not expressed in healthy proximal tubular
CC epithelium. The present invention relates to a hybridoma cell, and to progeny
CC specifically DSM ACC 2526, capable of producing Mab G250, and to progeny
CC cells produced e.g. by recombinant DNA methods. The invention also
CC relates to the use of the hybridoma cell and progeny cells for the
CC production of G250 antibodies, e.g. Mab, chimeric antibodies, (fully)
CC humanised antibodies, bispecific antibodies or chimeric fragments,
CC especially radiolabelled chimeric antibodies or chimeric antibodies
CC coupled to a cytokine such as Interleukin-2, tumour necrosis factor
CC and/or granulocyte-macrophage colony stimulating factor. A chimeric G250
CC antibody was successfully used in clinical studies for the treatment of
CC renal cell carcinoma cells after surgery. In some cases, tumour
CC regression occurred more than 6 months after start of therapy. Thus,
CC chimeric G250 antibody and other G250 antibodies are capable of eliciting
CC a delayed immune response in cancer therapy, preferably in the treatment
CC of renal cell carcinoma and more preferably in the treatment of
CC metastases after tumour surgery
XX
XX Sequence 357 BP; 86 A; 87 C; 94 G; 90 T; 0 U; 0 Other;
SQ

```

Alignment Scores:

```

Pred. No.: 1.12e-58 Length: 357
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

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US-10-635-908-6 (1-119) x ABO81172 (1-357)

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QY 1 AAPPVALLVLEUVALIGUSERGVYGLVYLVLEUVALVLEUVALVGLYSERLEUVALVLEU 20
DB 1 GAGGTAAAGCTCTGGAAGTCTGGGGAGGCTTAGTAGTGAAGCTTGGAGGCTCTCGAATC 60
QY 21 SerCYAALALASerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
DB 61 TCTGTGCAAGCCCTCGATTCACTTCAGTAACATTAATACATGCTTGGGTTCCCAAGCT 120
QY 41 ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
DB 121 CCAGAAAGAGGCTGAGAGTGTGCGAGCCATTAAATAGTATGTGTATACACTTACTAT 180
QY 61 LeuAspThrValAlaValGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
DB 181 CTAGAACTGTGAAGGCCGATTCACCATTTCAAGAGACAAATCCAGAAACACCTGTAC 240
QY 81 LeuGlnMetSerSerLeuValYsSerGluAspThrAlaLeuPheTyrCYAALALASArg 100
DB 241 CTCGAATATGAGAGTCTGGAAGTCTGAGAGACACAGCCCTGTTTATCTGTGCAAGACCGC 300
QY 101 SerGlyTyrPheSerMetAspTyrTyrPGLYGLNGlyThrSerValThrValSerSer 119

```

```

DB 301 ||||| 357
TCGGGCTACTTTCTATGACTCTGGGCTCAAGAACCTCAGTACCCCTCTCTCA
RESULT 2
ID ABO79691 standard; DNA; 357 BP.
XX ABO79691;
AC ABO79691;
XX
XX 05-DEC-2002 (first entry)
XX
XX G250 heavy chain variable region (VH G250) encoding DNA.
XX Antibody; antigen-binding site; diagnostic; therapeutic; radiolabeling;
XX cytotoxic; G250; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..357
XX FT /cseq= a
XX FT /product= "VH G250"
XX FT /partial
XX
XX MO200263010-A2.
XX
XX 15-AUG-2002.
XX
XX 07-FEB-2002; 2002WO-BP001283.
XX
XX 07-FEB-2001; 2001US-0266853P.
PR 05-OCT-2001; 2001US-0327008P.
XX
XX (WILE-) WILEX AG.
XX
XX Bolhuis RL, Weehl T, Boettger V;
XX WPI; 2002-627562/67.
XX P-PsDB; ABB82004.
XX
XX Novel nucleic acid sequence encoding antigen-binding site of the heavy or
PT light chain of an antibody useful for expressing the antibody suitable in
PT the field of tumor diagnostics and therapeutics.
XX
XX Claim 4; Fig 1; 18pp; English.
XX
XX The invention relates to novel nucleic acid (I) encoding the antigen-
CC binding site of the heavy or light chain of an antibody comprising a
CC nucleotide sequence encoding the CDR3 region. (I) is useful for the
CC recombinant production of a polypeptide having an antigen-binding site,
CC by introducing (I) into a mammalian cell, culturing the cell in a medium
CC where an expression of the nucleic acid takes place, and obtaining the
CC expressed product from the medium and/or the cell. Before introducing (I)
CC into the cell, the nucleic acid is modified so that the modification does
CC not alter the amino acid sequence of the antigen-binding site of the
CC polypeptide to be expressed. The expressed product, preferably antibodies
CC and antibody fragments are useful for preparing a diagnostic or
CC therapeutic agent and are coupled to a diagnostic marker or cytotoxic
CC agent. (I) is useful for expressing antibodies, e.g. chimerized
CC antibodies, humanized antibodies, heterobispecific antibodies, and single
CC chain antibodies, or antibody fragments. The expressed product can be
CC coupled to a diagnostic marker for use in in vitro diagnostic methods, or
CC radiolabeling procedures, or to a cytotoxic agent, e.g. a radionuclide, or
CC a toxin such as cholera toxin or ricin. The present sequence represents
CC G250 heavy chain variable region encoding DNA
XX
XX Sequence 357 BP; 86 A; 87 C; 94 G; 90 T; 0 U; 0 Other;
SQ

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Alignment Scores:

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Pred. No.: 1.12e-58 Length: 357
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

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Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0
US-10-635-908-6 (1-119) x ABQ79691 (1-357)

QY 1 AspVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuValLeu 20
DB 1 GACGTGAAGCTCGTGAAGCTGGGGGAGGCTTAGTGAAGCTTGAGAGGCTCCGAAACCTC 60

QY 21 SerCyAlAlAAseryGlyPheThrPheSerAsnTyTyTyrMetSertPValArgGlnThr 40
DB 61 TCCTGTGACACCTCGATTGACTTTCAGTAACTATTACATGCTTGGGTTCCGCAAGACT 120

QY 41 ProGluLyAsrGluLeuValAlAlAlAAsnSerAspGlyGlyIleThrTyTyTyr 60
DB 121 CCAGAGAGAGGCTGAGGTTGGTCGAGCATTATATGTAATGGTGTATCACCCTATAT 180

QY 61 LeuAspThrVallyGlyArgPheThrIleSerArgAspAsnAlAlAsanThrLeuTyTyr 80
DB 181 CTAGACACTGTGAAGGCCGATTCAACATTTCAGAGACATGCAAGAACACCCCTGTAC 240

QY 81 LeuGlnMetSerSerLeuLySerGlyAspThrAlAlLeuPheTyTyCysAlAArgHisArg 100
DB 241 CTGCAATATGAGCAGTCTGAAGCTGAGGACACAGCCCTGTGTTTACTGTGCAAGCACCGC 300

QY 101 SerGlyTyPheSerMetAspTyTyTyrGlyGlnGlyThySerValThrValSerSer 119
DB 301 TCGGGCTACTTTTCTATGACTACTGAGGCTCAGAGAACCTCAGTACCCGTCCTCA 357

RESULT 3
ABK43187
ID ABK43187 standard; DNA; 1056 BP.

AC ABK43187;
XX
XX 05-JUN-2002 (first entry)
XX
DE DNA encoding construct G250.
XX
XX Modified virus; adenovirus; cytostatic; gene therapy; tumour cell;
KW proliferating cell; cancer; vascular disease; inflammatory disease;
KW infectious disease; human immunodeficiency virus; HIV; gene; de.
XX
OS Human adenovirus type 5.
OS Synthetic.
XX
XX WO200208263-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-GB003252.
XX
XX 19-JUL-2000; 2000GB-00017720.
XX
XX (GOTA-) GOT-A-GENE AB.
XX
XX (GARD/) GARDNER R.
XX
XX Lindholm L, Nord AK, Boulanger PA;
XX
XX WPI; 2002-217049/27.
XX
XX P-PSDB; AAU87031.
XX
XX Novel modified virus comprising non-native polypeptides with stable
PT conformation and having framework moieties containing binding moieties
PT which confer upon the virus, an altered tropism, useful in gene therapy.
XX
XX Example 3; Page 95-99; 163pp; English.
XX
XX The invention describes a modified virus comprising non-native
CC polypeptides which has framework moieties each containing binding
CC moieties, where the virus has altered tropism conferred by the binding
CC moieties. The polypeptides can be expressed in the cytoplasm and nucleus
CC of mammalian host cell in conformation which is maintained in absence of

CC ligands for the binding moieties, where the conformation allows the
CC binding moiety subsequently to bind with the ligand. The modified virus
CC is useful in therapy for the preparation of a medicament for treating
CC tumour cells, cancer, proliferating cells, vascular diseases,
CC inflammatory diseases and infectious diseases such as Human
CC immunodeficiency virus (HIV). The altered tropisms allow the virus to be
CC used in treatment of disease in human or animal subjects, either by in
CC vivo treatment of, or ex vivo treatment of cells of, the subject
CC requiring treatment. The problems associated with the expression of
CC functional non-native viral components in the nucleus and cytosol of host
CC cells is solved by using the modified virus for the purpose. This
CC sequence encodes a protein sequence used in the creation of the modified
CC virus containing non-native polypeptides
XX
SQ Sequence 1056 BP; 268 A; 285 C; 271 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,026-58 Length: 1056
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-635-908-6 (1-119) x ABK43187 (1-1056)

QY 1 AspVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuValLeu 20
DB 376 GACGTGAAGCTCGTGAAGCTGGGGGAGGCTTAGTGAAGCTTGAGAGGCTCCGAAACCTC 435

QY 21 SerCyAlAlAAseryGlyPheThrPheSerAsnTyTyTyrMetSertPValArgGlnThr 40
DB 436 TCCTGTGACACCTCGATTGACTTTCAGTAACTATTACATGCTTGGGTTCCGCAAGACT 495

QY 41 ProGluLyAsrGluLeuValAlAlAlAAsnSerAspGlyGlyIleThrTyTyTyr 60
DB 496 CCAGAGAGAGGCTGAGGTTGGTCGAGCATTATATGTAATGGTGTATCACCCTATAT 555

QY 61 LeuAspThrVallyGlyArgPheThrIleSerArgAspAsnAlAlAsanThrLeuTyTyr 80
DB 556 CTAGACACTGTGAAGGCCGATTCAACATTTCAGAGACATGCAAGAACACCCCTGTAC 615

QY 81 LeuGlnMetSerSerLeuLySerGlyAspThrAlAlLeuPheTyTyCysAlAArgHisArg 100
DB 616 CTGCAATATGAGCAGTCTGAAGCTGAGGACACAGCCCTGTGTTTACTGTGCAAGCACCGC 675

QY 101 SerGlyTyPheSerMetAspTyTyTyrGlyGlnGlyThySerValThrValSerSer 119
DB 676 TCGGGCTACTTTTCTATGACTACTGAGGCTCAGAGAACCTCAGTACCCGTCCTCA 732

RESULT 4
ABK43189
ID ABK43189 standard; DNA; 1411 BP.

AC ABK43189;
XX
XX 05-JUN-2002 (first entry)
XX
XX
DE DNA encoding fiber construct A1 G250.
XX
XX Modified virus; adenovirus; cytostatic; gene therapy; tumour cell;
KW proliferating cell; cancer; vascular disease; inflammatory disease;
KW infectious disease; human immunodeficiency virus; HIV; gene; de.
XX
OS Human adenovirus type 5.
OS Synthetic.
XX
XX WO200208263-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-GB003252.
XX


```
PR 19-JUL-2000; 2000GB-00017720.
XX
XX (GOTA-) GOT-A-GENE AB.
PA (GARD/) GARDNER R.
XX
XX Lindholm L, Nord AK, Boulanger PA;
PI WPI; 2002-217049/27.
XX P-PSDB; AAU87033.
DR
XX Novel modified virus comprising non-native polypeptides with stable
PT conformation and having framework moieties containing binding moieties
PT which confer upon the virus, an altered tropism, useful in gene therapy.
XX
XX Example 3; Page 104-109; 163pp; English.
XX
XX The invention describes a modified virus comprising non-native
CC polypeptides which has framework moieties each containing binding
CC moieties, where the virus has altered tropism conferred by the binding
CC moieties. The polypeptides can be expressed in the cytoplasm and nucleus
CC of mammalian host cell in conformation which is maintained in absence of
CC ligands for the binding moieties, where the conformation allows the
CC binding moiety subsequently to bind with the ligand. The modified virus
CC is useful in therapy for the preparation of a medicament for treating
CC tumour cells, cancer, proliferating cells, vascular diseases,
CC inflammatory diseases and infectious diseases such as Human
CC immunodeficiency virus (HIV). The altered tropisms allow the virus to be
CC used in treatment of disease in human or animal subjects, either by in
CC vivo treatment of, or ex vivo treatment of cells of, the subject
CC requiring treatment. The problems associated with the expression of
CC functional non-native viral components in the nucleus and cytosol of host
CC cells is solved by using the modified virus for the purpose. This
CC sequence encodes a protein sequence used in the creation of the modified
CC virus containing non-native polypeptides
XX
SQ Sequence 1411 BP; 363 A; 391 C; 349 G; 308 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 5.65e-58 Length: 1411
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-635-908-6 (1-119) x ABK43190 (1-1411)
QY 1 AspValIysLeuValGluSerGIyGIyGlyLeuValIysLeuGIySerLeuIysLeu 20
Db 722 GACGTAAAGCTCGTGAAGTCTGGGAGGCTTAGTGAAGCTTGGAAGGTCCTCGAAACATC 781
QY 21 SerCyAlAlAlAserGIyPheThrPheSerAenTyTYTMeSerTrpValArgIntnr 40
Db 782 TCCTGGAGCCCTCGATTCACCTTCAGTAACATTAATGCTTCGGGTCCCGACACT 841
QY 41 ProGluIysArgIleuGIyLeuValAlAlAlAserSerAspGIyGIyIleThrTYTYX 60
Db 842 CCAGAGAAAGGCTGGAAGTGTGGCAGCATTAAATGATGATGATGATGATGATGATGATGAT 901
QY 61 LeuAspThrValIysGIyArgPheThrIleSerArgAspAsnAlAlAsenThrIysLeu 80
Db 902 CTAGACACGTGTGAAGGCCGATTCACCATTTCAAGACACATGCCAGAAACCCCTGTAC 961
QY 81 LeuGIyMetSerSerLeuIysSerGIyAspThrAlAlLeuPheTyTCyAlAlArgIlsArg 100
Db 962 CTGCAATATGAGCAGTCTGAAGTCTGAGGACACAGCCCTGTGTTACTGTGCAAGACACCG 1021
QY 101 SerGIyTYrPheSerMetAspTYRTTGGIyGInGIyThSerValThrValSerSer 119
Db 1022 TCGGGCTACTTTTCTATGACTACTGGGGTCAAGAAACCTCAACCTGCTCTCTCA 1078
RESULT 5
ABK43190
```

```
ID ABK43190 standard; DNA; 1702 BP.
XX
XX AC ABK43190;
XX
XX 05-JUN-2002 (first entry)
XX
XX DE DNA encoding fiber construct A7 G250.
XX
XX KW Modified virus; adenovirus; cytostatic; gene therapy; tumour cell;
KW proliferating cell; cancer; vascular disease; inflammatory disease;
KW infectious disease; human immunodeficiency virus; HIV; gene; ds.
XX
XX OS Human adenovirus type 5.
XX
XX OS Synthetic.
XX
XX PN WO200208263-A2.
XX
XX PD 31-JAN-2002.
XX
XX PF 19-JUL-2001; 2001WO-GB003252.
XX
XX PR 19-JUL-2000; 2000GB-00017720.
XX
XX PA (GOTA-) GOT-A-GENE AB.
XX (GARD/) GARDNER R.
XX
XX PI Lindholm L, Nord AK, Boulanger PA;
XX WPI; 2002-217049/27.
XX P-PSDB; AAU87034.
DR
XX Novel modified virus comprising non-native polypeptides with stable
PT conformation and having framework moieties containing binding moieties
PT which confer upon the virus, an altered tropism, useful in gene therapy.
XX
XX Example 3; Page 109-116; 163pp; English.
XX
XX The invention describes a modified virus comprising non-native
CC polypeptides which has framework moieties each containing binding
CC moieties, where the virus has altered tropism conferred by the binding
CC moieties. The polypeptides can be expressed in the cytoplasm and nucleus
CC of mammalian host cell in conformation which is maintained in absence of
CC ligands for the binding moieties, where the conformation allows the
CC binding moiety subsequently to bind with the ligand. The modified virus
CC is useful in therapy for the preparation of a medicament for treating
CC tumour cells, cancer, proliferating cells, vascular diseases,
CC inflammatory diseases and infectious diseases such as Human
CC immunodeficiency virus (HIV). The altered tropisms allow the virus to be
CC used in treatment of disease in human or animal subjects, either by in
CC vivo treatment of, or ex vivo treatment of cells of, the subject
CC requiring treatment. The problems associated with the expression of
CC functional non-native viral components in the nucleus and cytosol of host
CC cells is solved by using the modified virus for the purpose. This
CC sequence encodes a protein sequence used in the creation of the modified
CC virus containing non-native polypeptides
XX
XX SQ Sequence 1702 BP; 447 A; 494 C; 404 G; 357 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 7.05e-58 Length: 1702
Score: 617.00 Matches: 119
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-635-908-6 (1-119) x ABK43190 (1-1702)
QY 1 AspValIysLeuValGluSerGIyGIyGlyLeuValIysLeuGIySerLeuIysLeu 20
Db 1013 GACGTAAAGCTCGTGAAGTCTGGGAGGCTTAGTGAAGCTTGGAAGGTCCTCGAAACATC 1072
QY 21 SerCyAlAlAlAserGIyPheThrPheSerAenTyTYTMeSerTrpValArgIntnr 40
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DB 1073 TCCTGTGCACCTCTGGATTCACTTTCAGTAACTATACATGCTGGTCCAGACT 1132
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60
DB 1133 CCAGAGAAAGAGCGCTGGAGTGTGCTGCAGCATTAATGTATGATGGTATACCTACTAT 1192
QY 61 LeuAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
DB 1193 CTAGACACTGTGAAGGCCCATTCACATTTCAAGAGACAAATGCCAAGAACCCCTGTAC 1252
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
DB 1253 CTGCAAAATGAGCACTCGAAGTCTGAGAGACACAGCCCTGTTTACTGTGCAGACACCGC 1312
QY 101 SerGlyTyrPheSerMetAspTyrTTPGlyGlnGlyThrSerValThrValSerSer 119
DB 1313 TCGGGCTACTTTTCTATGACTACTGGGGTCMAAGAACTTCAGTCACCGTCTCTCA 1369
RESULT 6
ADC24965
ID ADC24965 standard; DNA, 444 BP.
XX
AC ADC24965;
XX
DT 18-DEC-2003 (first entry)
XX
DE Murine G250 heavy chain variable region DNA SEQ ID NO:50.
XX
KW fusion protein; chimerised antibody; tumour necrosis factor; TNF;
KW antibody; chimeric fusion protein; antiinflammatory; antirheumatic;
KW antiarthritic; antipsoriatic; antiaesthetic; neuroprotective; virocid;
KW antibacterial; immunosuppressive; nephrotoxic; antiarteriosclerotic;
KW rheumatoid arthritis; inflammatory condition; psoriasis; asthma;
KW inflammatory bowel disease; multiple sclerosis; viral pneumonia;
KW bacterial pneumonia; septic shock; nephritis; arteriosclerosis; mouse;
KW gene; ds.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO2003068924-A2.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2003; 2003WO-US004243.
XX
PR 13-FEB-2002; 2002US-0355838P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Renner C, Scott A;
XX
DR MPI; 2003-679629/64.
XX
DR P-PSDB; ADC24966.
XX
PT New nucleic acid, useful for producing humanized or chimeric antibodies,
PT or fusion proteins comprising the antibodies, which are G250-specific and
PT useful for treating inflammatory conditions, e.g. rheumatoid arthritis or
PT asthma.
XX
PS Example 16; SEQ ID NO 50; 80pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC encodes a fusion protein comprising a chimerised antibody molecule, and a
CC tumour necrosis factor (TNF) molecule or its fragment. The antibody
CC specifically binds to a target. The fragment of the TNF molecule
CC possesses the cell killing properties of a full-length TNF molecule. Also
CC described: (1) a chimeric fusion protein (I) encoded by the isolated
CC nucleic acid molecule; (2) an expression vector comprising the isolated
CC nucleic acid molecule operably linked to a promoter; and (3) a
CC recombinant cell comprising the isolated nucleic acid molecule or the
CC expression vector. (I) has antiinflammatory, antirheumatic,
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CC antiarthritic, antipsoriatic, antiaesthetic, neuroprotective, virocid,
CC antibacterial, immunosuppressive, nephrotoxic and antiarteriosclerotic
CC activities. The nucleic acid is useful for the expression of proteins,
CC especially antibodies, as well as fusion proteins that incorporate the
CC antibody and a protein. The expression vector is useful in manufacturing
CC a recombinant antibody (e.g. a fully human, humanized or chimeric
CC antibody) in a eukaryotic cell. The antibody is useful in therapy.
CC particularly for targeting G250 and blocking granulocyte-macrophage
CC stimulating factor (GM-CSF), which is involved in the development of
CC rheumatoid arthritis. The antibody is useful for treating inflammatory
CC conditions, e.g. psoriasis, asthma, inflammatory bowel disease, multiple
CC sclerosis, viral or bacterial pneumonia, septic shock, nephritis, or
CC arteriosclerosis. The present sequence encodes murine G250 antibody heavy
CC chain variable region, which is used in an example from the present
CC invention.
XX
SQ Sequence 444 BP; 103 A; 108 C; 114 G; 119 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3e-57 Length: 444
Score: 605.00 Matches: 117
Percent Similarity: 98.3% Conservative: 0
Best Local Similarity: 98.3% Mismatches: 2
Query Match: 98.1% Indels: 0
DB: Gaps: 10
XX
US-10-635-908-6 (1-119) x ADC24965 (1-444)
QY 1 AspValLysLeuValAlaGluSerGlyGlyLeuValLysLeuValSerLeuValLeu 20
DB 75 GAGGTGAAGCTCGTGGAGCTGGGGCAGCGCTTGTGAAGCTTGGAGGGTCCCTGAATC 134
QY 21 SerCysAlaIleAsnSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgIleThr 40
DB 135 TCCTGTGCACCTCTGGATTCACTTTCAGTAACTATACATGCTGGTCCAGACT 194
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyr 60
DB 195 CCAGAGAAAGAGCGCTGGAGTGTGCTGCAGCATTAATGTATGATGGTATACCTACTAT 254
QY 61 LeuAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
DB 255 CTAGACACTGTGAAGGCCCATTCACATTTCAAGAGACAAATGCCAAGAACCCCTGTAC 314
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
DB 315 CTGCAAAATGAGCACTCGAAGTCTGAGAGACACAGCCCTGTTTACTGTGCAGACACCGC 374
QY 101 SerGlyTyrPheSerMetAspTyrTTPGlyGlnGlyThrSerValThrValSerSer 119
DB 375 TCAAGCTACTTTTCTATGACTACTGGGGTCMAAGAACTTCAGTCACCGTCTCTCA 431
RESULT 7
ADK51720
ID ADK51720 standard; DNA, 444 BP.
XX
AC ADK51720;
XX
DT 06-MAY-2004 (first entry)
XX
DE Murine G250 variable heavy chain region cDNA.
XX
KW granulocyte macrophage colony stimulating factor; GM-CSF; antibody;
KW antiinflammatory; antiarthritic; antirheumatic; rheumatoid arthritis;
KW inflammatory disease; murine; mouse; G250; gene; ss.
XX
OS Mus sp.
XX
PN WO2003068920-A2.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2003; 2003WO-US004185.
```

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XX
PR 13-FEB-2002; 2002US-0356838P.
XX
XX (LUDM-) LUDMIG INST CANCER RES.
XX
XX Renner C, Scott A, Burgess A;
XX
XX WPI: 2003-679625/64.
XX
XX P-PSDB; ADRS1721.
XX
XX Nucleic acids encoding chimeric granulocyte macrophage colony stimulating
XX factor (GM-CSF) specific antibodies comprising a light and a heavy chain,
XX useful for blocking effects of GM-CSF on cells, e.g. in preventing
XX rheumatoid arthritis.
XX
XX Example 16; SEQ ID NO 50; 81pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a chimerised
XX granulocyte macrophage colony stimulating factor (GM-CSF) specific
XX antibody light chain or heavy chain. The invention further relates to: a
XX chimerised granulocyte macrophage colony stimulating factor (GM-CSF)
XX specific antibody light chain encoded by nucleotides 1357-1752 of a
XX defined sequence of 6159 bp concatenated to the amino acid sequence
XX encoded by nucleotides 1886-2203 of the 6159bp sequence; or a chimerised
XX GM-CSF specific antibody heavy chain encoded by nucleotides 1357-1764 of
XX a defined 6629 bp sequence concatenated to the amino acid sequence
XX encoded by nucleotides 1839-2825 of the 6629bp sequence. The GM-CSF
XX antibodies have antiinflammatory, antiarthritic, and antirheumatic
XX activities. The GM-CSF nucleic acid is useful for blocking GM-CSF and its
XX effects on cells, such as in preventing the development of rheumatoid
XX arthritis and other inflammatory diseases and conditions. This
XX polynucleotide sequence represents the cDNA of a murine G250 heavy chain
XX variable region protein of the invention.
XX
XX Sequence 444 BP; 103 A; 108 C; 114 G; 119 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 3e-57 Length: 444
XX Score: 605.00 Matches: 117
XX Percent Similarity: 98.3% Conservative: 0
XX Best Local Similarity: 98.3% Mismatches: 2
XX Query Match: 98.1% Indels: 0
XX DB: 10 Gaps: 0
XX
XX US-10-635-908-6 (1-119) x ADRS1720 (1-444)
XX
XX 1 AspValIlyLeuValIgluSerGlyGlyLeuValIlyLeuGlyIySerLeuValLeu 20
XX 75 GACGTGAAGCTCGTGAAGTCTGGGGCAGCCTTAGTAAGCTTGGAGGGTCCCGAATC 134
XX
XX 21 SerCyAlAlAlaserGlyPheThrPheSerAantTtYtMetSerTtPValArgGInttr 40
XX 135 TCTGTGACGACCTTGATTCACCTTCAGTAACCTATTACATGCTGGGTCCCGAGACT 194
XX
XX 41 ProGluLyArGheGluLeuValAlAlAlAlAsmSerApsGlyGlyIleThrYtYtYr 60
XX 195 CCAAGAAAGAGGCTGAGATTGTCGACGACCATTAATGATGATGATGATGATGATGAT 254
XX
XX 61 LeuAepThrValIlysgIyArGheThrIleSerArGAspAnaAlAlYsAntThrIleYtYr 80
XX 255 CTGACACACTGTGAAAGGCGCATTCACCATTTCAAGAGACAAATGCCAAGAACCCCTGTAC 314
XX
XX 81 LeuGImetSerSerLeuYsSerGluAepThrAlAlaLeuPheYtCyAlAlAghIleAag 100
XX 315 CTGCAATATGAGCTGAGAGTCTGAGAGACAGCCCTGTGTTTAACTGTGCAAAACCCGC 374
XX
XX 101 SerGlyTyRPhesermetAepTYtTPGlyGInGlyThsSerValThrValSerSer 119
XX 375 TCAGGCTACTTTCTATGACCTACTGGGTCAAAGAACCTCAATCACCCTCTCTCA 431
XX
XX
XX RESULT 8
XX ABO79699
XX ID ABO79699 standard; DNA; 2431 BP.
```

```
XX
XX ABO79699;
XX
XX 05-DEC-2002 (first entry)
XX
XX G250 heavy chain variable region (HC_G250) DNA fragment.
XX
XX Antibody; antigen-binding site; diagnostic; therapeutic; radiolabeling;
XX cytotoxic; G250; ds.
XX
XX Homo sapiens.
XX
XX MO200263010-A2.
XX
XX 15-AUG-2002.
XX
XX 07-FEB-2002; 2002WO-EP001283.
XX
XX 07-FEB-2001; 2001US-0266853P.
XX
XX 05-OCT-2001; 2001US-0327008P.
XX
XX (WILE-) WILEX AG.
XX
XX Bolhuis RL, Woehl T, Boettger V;
XX
XX WPI; 2002-627562/67.
XX
XX Novel nucleic acid sequence encoding antigen-binding site of the heavy or
XX light chain of an antibody useful for expressing the antibody suitable in
XX the field of tumor diagnostics and therapeutics.
XX
XX Example 2; Fig 3A; 18pp; English.
XX
XX The invention relates to novel nucleic acid (I) encoding the antigen-
XX binding site of the heavy or light chain of an antibody comprising a
XX nucleotide sequence encoding the CDR3 region. (I) is useful for the
XX recombinant production of a polypeptide having an antigen-binding site,
XX by introducing (I) into a mammalian cell, culturing the cell in a medium
XX where an expression of the nucleic acid takes place, and obtaining (I)
XX expressed product from the medium and/or the cell. Before introducing (I)
XX into the cell, the nucleic acid is modified so that the modification does
XX not alter the amino acid sequence of the antigen-binding site of the
XX polypeptide to be expressed. The expressed product, preferably antibodies
XX and antibody fragments are useful for preparing a diagnostic or
XX therapeutic agent and are coupled to a diagnostic marker or cytotoxic
XX agent. (I) is useful for expressing antibodies, e.g. chimerised
XX antibodies, humanized antibodies, heterodispecific antibodies, and single
XX chain antibodies, or antibody fragments. The expressed product can be
XX coupled to a diagnostic marker for use in in vitro diagnostic methods, or
XX radioimaging procedures, or to a cytotoxic agent, e.g. a radionuclide, or
XX a toxin such as cholera toxin or ricin. The present sequence represents
XX G250 heavy chain variable region DNA fragment HC_G250 (Bc0R1-fragment in
XX expression vector)
XX
XX Sequence 2431 BP; 720 A; 455 C; 552 G; 698 T; 0 U; 6 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1.31e-55 Length: 2431
XX Score: 598.00 Matches: 115
XX Percent Similarity: 97.5% Conservative: 1
XX Best Local Similarity: 96.6% Mismatches: 3
XX Query Match: 96.9% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-10-635-908-6 (1-119) x ABO79699 (1-2431)
XX
XX 1 AspValIlyLeuValIgluSerGlyGlyLeuValIlyLeuGlyIySerLeuValLeu 20
XX 843 GACGTGAAGCTCGTGAAGTCTGGGGCAGCCTTAGTAAGCTTGGAGGGTCCCGAATC 902
XX
XX 21 SerCyAlAlAlaserGlyPheThrPheSerAantTtYtMetSerTtPValArgGInttr 40
XX 903 TCTGTGACGACCTTGATTCACCTTCAGTAACCTATTACATGCTGGGTCCCGAGACT 962
XX
XX
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```

QY 41 ProGluLyArGrLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
DB 963 CCAGAGAGAGGCTGGAGTTGGTCGCANNATTAANNNTGATGTGTATCAGCTTCTAT 1022
QY 61 LeuAspThrValLySglYArGrPheThrIleSerArgAspAsnAlaLySaenThrLeuTYr 80
DB 1023 CTAGACACTGTGAAGGCCGATTCAACCATTTCAAGAGACAATGCCAAGAACACCTGTAC 1082
QY 81 LeuGlnMetSerSerLeuLySergIuAspThrAlaLeuPheTYrCYsaIaArgHisArg 100
DB 1083 CTCCAATATGACGAGTCTGAAGTCTGAGACACAGCCCTGTATTACTGTGCAAGACACCGC 1142
QY 101 SerGlyThrPheSerMetAspTYrTPGlyGlnGlyThrSerValThrValSerSer 119
DB 1143 TCGGGACTTTCCTATGACACTGCTGGGGTCAGAGAACTTCAGTCAACCTGCTCTCA 1199

RESULT 9
AAT70808
ID AAT70808 standard; DNA; 474 BP.
AC AAT70808;
DT 30-JUL-1997 (first entry)
XX
DE Mouse anti-idiotypic antibody 3B6 heavy chain variable region.
KW Anti-idiotypic; anti-BGFR; epidermal growth factor receptor; tumour;
KM cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
XX
OS Mus musculus.
FH
FH Key Location/Qualifiers
FT CDS 1..474
FT /*tag= a
FT /transl_except= pos:388..390, aa: Ala
FT /note= "no stop codon given"
FT sig_peptide 1..57
FT primer_bind 1..30
FT /*tag= c
FT primer_bind 448..474
FT /*tag= d
PN EP745612-A1.
XX
XX 04-DEC-1996.
XX
XX 14-MAY-1996; 96EP-00107651.
XX
XX 26-MAY-1995; 95EP-00107967.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Carceller A, Rosell E, Gomez A, Adan J, Piuilats J;
XX
XX WPI, 1997-013659/02.
XX
XX P-PSDB; AAM19577.
XX
XX Monoclonal anti-idiotypic antibodies mimicking epidermal growth factor
XX receptor - useful for tumour therapy.
XX
XX Claim 6; Fig 5C; 28pp; English.
XX
XX Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are new.
XX They induce an immune response against epidermal growth factor receptor
XX (EGFR). The sequences of the heavy and light chain variable regions of
XX these antibodies are given in the specification. The antibodies are used
XX for the manufacture of drugs directed against tumours that express EGFR
XX on their surface, including melanomas, gliomas and carcinomas
XX
XX Sequence 474 BP; 112 A; 119 C; 122 G; 121 T; 0 U; 0 Other;
SQ

```

```

Alignment Scores:
Pred. No.: 1.7e-52 Length: 474
Score: 562.00 Matches: 112
Percent Similarity: 92.8% Conservative: 4
Beet Local Similarity: 89.6% Mismatches: 3
Query Match: 91.1% Indels: 6
DB: 2 Gaps: 2

US-10-635-908-6 (1-119) x AAT70808 (1-474)
QY 1 AspValLyLeuValGluSerGlyGlyLeuValLyLeuGlyLYSerLeuLYLeu 20
DB 58 GACGTAAAGCTCGTGAAGTCTGGGGAGCTTAGTAAGCTTGAGAGGTCCTGGAATC 117
QY 21 SerCYsaIaIaSerGlyPheThrPheSerAsnTYrTYrMetSerTPYValArgGlnThr 40
DB 118 TCTGTGACAGCCCTGTGATTCATCTTCAGTAACATTAATGATGCTGGGTCCGACAGCT 177
QY 41 ProGluLyArGrLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
DB 178 CCAGAGAGAGGCTGGAGTGTTCGACGCCATTAAATAGTAATGTGTGACACCTTACTAT 237
QY 61 LeuAspThrValLySglYArGrPheThrIleSerArgAspAsnAlaLySaenThrLeuTYr 80
DB 238 CCAGACACTGTGAAGGCCGATTCAACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 297
QY 81 LeuGlnMetSerSerLeuLySergIuAspThrAlaLeuPheTYrCYsaIaArgHisArg 100
DB 298 CTCCAATATGACGAGTCTGAAGTCTGAGACACAGCCCTGTATTACTGTGCAAGACATCGG 357
QY 101 -----SerGlyTYr-----PheSerMetAspTYrTPGlyGlnGlyThrSer 114
DB 358 GGGAGGAGACGCTCGGGCTACGTAGGGTATTCTATAGACTACGGGGTCAAGAACTCA 417
QY 115 ValThrValSerSer 119
DB 418 GTCACCGTCTCTCA 432

RESULT 10
AAT70810
ID AAT70810 standard; DNA; 474 BP.
AC AAT70810;
DT 30-JUL-1997 (first entry)
XX
XX
DE Mouse anti-idiotypic antibody 5A6 heavy chain variable region.
XX
XX Anti-idiotypic; anti-BGFR; epidermal growth factor receptor; tumour;
XX cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
XX
XX
OS Mus musculus.
FH
FH Key Location/Qualifiers
FT CDS 1..474
FT /*tag= a
FT /note= "no stop codon given"
FT sig_peptide 1..57
FT primer_bind 1..25
FT /*tag= c
FT primer_bind 448..474
FT /*tag= d
PN EP745612-A1.
XX
XX 04-DEC-1996.
XX
XX 14-MAY-1996; 96EP-00107651.
XX
XX 26-MAY-1995; 95EP-00107967.
XX
XX (MERE ) MERCK PATENT GMBH.
XX

```

XX Carceller A, Rosell E, Gomez A, Adan J, Pinlata J;
XX WPI; 1997-013659/02.
DR P-PsDB; AAM19579.
XX
XX Monoclonal anti-idiotypic antibodies mimicking epidermal growth factor
PT receptor - useful for tumour therapy.
XX
XX Claim 6; Fig 5E; 28pp; English.
XX
XX Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are new.
CC They induce an immune response against epidermal growth factor receptor
CC (EGFR). The sequences of the heavy and light chain variable regions of
CC these antibodies are given in the specification. The antibodies are used
CC for the manufacture of drugs directed against tumours that express EGFR
CC on their surface, including melanomas, gliomas and carcinomas
XX
SQ Sequence 474 BP; 110 A; 117 C; 125 G; 122 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.63e-52 Length: 474
Score: 559.00 Matches: 111
Percent Similarity: 92.8% Conservative: 5
Best Local Similarity: 80.8% Mismatches: 3
Query Match: 90.6% Indels: 6
DB: Gaps: 2

US-10-635-908-6 (1-119) x AAT70810 (1-474)

QY 1 AapvallyleuValGluSerGlyGlyLeuVallyleuGlyGlySerleuLysLeu 20
DB 58 GACGTAAAGCTCTGAGAGCTGAGGAGGCTTGTAAAGCTTGAAGGCTCCCGAAACTA 117
QY 21 SerCyAAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
DB 118 TCCTGTGACAGCTCTGATTCACCTTCAGTAATTAATTAATTAATTAATTAATTAATTA 177
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
DB 178 CCAGAAAGAGCTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAG 237
QY 61 LeuAspThrValIlyGlyArgPheThrIleSerArgAspAsnAlaIlyAsnThrLeuTyr 80
DB 238 CCAGACACTGTGAAGGCGCATTCACCATCTCCAGAGACATCCAGAAACCCCTGTAC 297
QY 81 LeuGlnMetSerSerleuLysSerGluAspThrAlaLeuPheTyrCyAAlaArgHisArg 100
DB 298 CTGCAATGAGAGCTGAGAGCTGAGAGACACAGCCCTGTATTAATTAATTAATTAATTA 357
QY 101 -----SerGlyTyr-----PheSerMetAspTyrTyrGlyGlnGlyThrSer 114
DB 358 GGGAGGAGACAGCTCGGAGCTTACGTAGGGTATGATTAAGTACTACTGGGCTCAAGAACTCA 417
QY 115 ValThrValSerSer 119
DB 418 GTCAACCTCTCTCA 432

RESULT 11

AAC90629 ID AAC90629 standard; DNA; 422 BP.

XX AAC90629;

XX 20-MAR-2001 (first entry)

XX Plasmid gamma1WT-TAC sequence.

XX Somatic transgene immunisation; immune response; haematopoietic cell;
XX immunity; disease treatment; disease prevention; ds.
XX Synthetic.
XX

PN WO20064488-A2.
XX
XX 02-NOV-2000.
XX
XX 27-APR-2000; 2000WO-US011372.
XX
XX 27-APR-1999; 99US-00300959.
XX
XX (ZANE/) ZANETTI M.
XX
XX Zanetti M;
XX
XX WPI; 2001-024628/03.
XX
XX Immunization by administering ex vivo a transgene having a hematopoietic
PT cell-specific expression element operationally linked to a polynucleotide
PT encoding one or more heterologous epitopes to a lymphoid cell.
XX
XX Example 1; Fig 2; 100pp; English.
XX

CC The present invention provides a novel method of immunisation involving
CC the administration of a haematopoietic cell specific expression element
CC to a lymphoid cell. The method is known as somatic transgene
CC immunisation. It is particularly useful in the treatment and prevention
CC of tumours, autoimmune diseases, allergy, metabolic disorders, endocrine
CC disorders, mental disorders, pain, blood disorders and dental disorders
XX
SQ Sequence 422 BP; 103 A; 98 C; 110 G; 111 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.91e-49 Length: 422
Score: 532.00 Matches: 106
Percent Similarity: 90.8% Conservative: 2
Best Local Similarity: 89.1% Mismatches: 11
Query Match: 86.2% Indels: 0
DB: Gaps: 0

US-10-635-908-6 (1-119) x AAC90629 (1-422)

QY 1 AapvallyleuValGluSerGlyGlyLeuVallyleuGlyGlySerleuLysLeu 20
DB 1 GACGTAAAGCTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAG 60
QY 21 SerCyAAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
DB 61 TCCTGTGACAGCTCTGATTCACCTTCAGTAATTAATTAATTAATTAATTAATTAATTA 120
QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
DB 121 CCAGAAAGAGCTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAG 180
QY 61 LeuAspThrValIlyGlyArgPheThrIleSerArgAspAsnAlaIlyAsnThrLeuTyr 80
DB 181 CCAGACACTGTGAAGGCGCATTCACCATCTCCAGAGACATCCAGAAACCCCTGTAC 240
QY 81 LeuGlnMetSerSerleuLysSerGluAspThrAlaLeuPheTyrCyAAlaArgHisArg 100
DB 241 CTGCAATGAGAGCTGAGAGCTGAGAGACACAGCCCTGTATTAATTAATTAATTAATTA 300
QY 101 SerGlyTyrPheSerMetAspTyrTyrGlyGlnGlyThrSerValThrValSerSer 119
DB 301 CCTACTCTCATGTATGAGTACTAGGGGTCAAGAAACCTCAAGTACCGCTCTCTCA 357

RESULT 12

AAT91614 ID AAT91614 standard; CDNA to mRNA; 735 BP.

XX AAT91614;

XX 22-DEC-1997 (first entry)

XX CDNA encoding an anti-T3 antibody derived scFv.
XX
XX


```

DB      64 TGTGAAGCCTGTGATTCATTGATTTATATGATCTTGGGTTCCAGACTCCA 123
OY      42 GIUYSARGLEUGLNULEUVALAALALEANSERAPGLYGLYLLETHRYTYRLEU 61
DB      124 GAGAGAGGCTGAGAGTGTGCTCCAGCCATTATAGTAATGTGTGTAACACTTATTTCA 183
OY      62 AAPTNRVALLEGLIYARGPHERTHRIIIESERARGAPASNAIAYASANTHRLEUYRLEU 81
DB      184 GACACTGTGAAGGCGGATTCACATCTCCAGAGCAATGCCAAGAACACCCGTGACTCG 243
OY      82 GINMESERSEULEUSERGILUAPETHRALALEUPHETRYCYBALARGHISARGSER 101
DB      244 CAAATGAGCAGTCTGAAAGTCTGAGACACAGCCTGTATTACTGTGCAACCCGCTCTCC 303
OY      102 GLYTYR-----PheserMeaApTYRTTPGLYGLINGLYTHRSERVALTHRSER 119
DB      304 TATTATTACCTCTATGTCATGTACTACTGGGGCCAAAGGACACGCTCACCGTCTCTCA 363

RESULT 14
AAV11906 standard; cDNA to mRNA, 354 BP.
XX
AC      AAV11906;
XX
DT      13-AUG-1998 (first entry)
XX
DE      Mouse PAF receptor antibody heavy chain hypervariable region cDNA.
XX
KW      Immunoglobulin heavy chain; hypervariable region; PAF; CDR; antibody;
XX      platelet activating factor receptor; murine; ds.
XX
OS      Mus sp.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..354
FT      FT      /*tag= a
FT      FT      /codon_start= 3
FT      FT      /product= "PAF receptor antibody heavy chain
FT      FT      hypervariable region"
FT      FT      /note= "partial coding sequence"
XX
PN      JP10136981-A.
XX
PD      26-MAY-1998.
XX
PF      12-NOV-1996; 96JP-00317047.
XX
PR      12-NOV-1996; 96JP-00317047.
XX
PA      (SUME ) SUMITOMO ELECTRIC IND CO.
XX
DR      WPI; 1998-355043/31.
XX      P-PSDB; AAMS9167.
XX
PT      Polypeptide comprising variable region of antibody recognising PAF
XX      receptor - useful for the preparation of chimeric antibody.
XX
PS      Disclosure; Page 8; 14pp; Japanese.
XX
CC      This sequence encodes the heavy chain hypervariable region of an antibody
CC      recognising the platelet activating factor (PAF) receptor. The variable
CC      region of mouse anti-PAF receptor monoclonal antibody is useful for the
CC      preparation of chimeric antibodies
XX
SQ      Sequence 354 BP; 88 A; 83 C; 95 G; 88 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      4.64e-46      Length:      354
Score:      502.00      Matches:      99
Percent Similarity: 89.7%      Conservative: 6
Best Local Similarity: 84.6%      Mismatches: 12
Query Match:      81.4%      Indels:      0

```

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DB:      2      Gaps:      0
US-10-635-908-6 (1-119) x AAV11906 (1-354)
OY      2 VALLYSLEUVALIGUSERGLYGLYLEUVALLYSLEUGLYGLYSERLEUYSLEUSER 21
DB      3 GTGAAGCTCCAGAGAGTCTGGGGAGGCTTAGGAAACTTGGAGGGTCCCTTAAACTCTCC 62
OY      22 CYBALAALASERGLYPHERTHRPHESERANTYRYTYRMESERTTPVALARGGLNTHRPRO 41
DB      63 TGTGACGCTCTGATTCATTGAGTACTTATTCATGTCCTTGGGTTCCAGACTCCA 122
OY      42 GIUYSARGLEUGLNULEUVALAALALEANSERAPGLYGLYLLETHRYTYRLEU 61
DB      123 GAGAAAGGCTGAAATTTGCTCCAGCCATTATAGTAATGTGTATTAACACTTATTTCA 182
OY      62 AAPTNRVALLEGLIYARGPHERTHRIIIESERARGAPASNAIAYASANTHRLEUYRLEU 81
DB      183 GACAAATGTAAGGCGGATTCACATCTCCAGAGCAATGCCAAGAACACCCGTGACTCG 242
OY      82 GINMESERSEULEUSERGILUAPETHRALALEUPHETRYCYBALARGHISARGSER 101
DB      243 CAAATGAGCAGTCTGAGGCTGAGACACATTCCTGTATTATTGTGCCAAGACCTGTGACT 302
OY      102 GLYTYRPHESERMEASPTTYRTTPGLYGLINGLYTHRSERVALTHRSER 118
DB      303 AGTTACGCTGTGTTGATCATCTGGGGCCAAAGGACACGCTCACCGTCTTC 353

RESULT 15
ABZ21159 standard; DNA, 366 BP.
XX
AC      ABZ21159;
XX
DT      28-MAR-2003 (first entry)
XX
DE      Variable region anti-bisphenol A antibody chain coding sequence #3.
XX
KW      Variable region; anti-bisphenol A; antibody; murine; heavy chain;
XX      light chain; gene; ds.
XX
OS      Mus sp.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..366
FT      FT      /*tag= a
FT      FT      /partial
FT      FT      /product= "Variable region anti-bisphenol A antibody
FT      FT      chain #3"
FT      FT      /note= "No start or stop codon given"
XX
PN      JP2002253259-A.
XX
PD      10-SEP-2002.
XX
PF      02-MAR-2001; 2001JP-00058673.
XX
PR      02-MAR-2001; 2001JP-00058673.
XX
PA      (BIOS-) BIO APPLIED SYSTEMS KK.
XX
DR      WPI; 2003-096537/09.
XX      P-PSDB; ABB98907.
XX
PT      Gene encoding anti-bisphenol A antibody, a recombinant protein and its
XX      preparation, a DNA, a vector, a transformant, preparation of a
XX      recombinant protein, a kit for determining bisphenol A.
XX
PS      Claim 1; Page 12; 19pp; Japanese.
XX
CC      The present invention relates to sequences for murine heavy chain
XX      variable region or light chain variable region of anti-bisphenol A
XX      antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are

```


CC useful for the preparation of recombinant protein
XX
SQ Sequence 366 BP; 86 A; 88 C; 99 G; 93 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.05e-46	Length:	366
Score:	500.50	Matches:	100
Percent Similarity:	86.9%	Conservative:	6
Best Local Similarity:	82.0%	Mismatches:	13
Query Match:	81.1%	Indels:	3
DB:	8	Gaps:	2

US-10-635-908-6 (1-119) x ABZ21159 (1-366)

```
QY      1 AspValIlyLeuValGIuSerGIyGIyLeuValIlySerLeuIySerLeu 20
      |||
      1 GACGTGAAGTTCGTGGAGGCTTGAAGCTTGAAGGCTCCGAAACTC 60
QY      21 SerCysAlaIaSerGIyPheThrPheSerAsnTyTYrMetSerTPValArgInThr 40
      |||
      61 TCATGTCCAGCCCTCTGGAATTCATTGAAACTATTACATGCTTGGTTCCGCAACT 120
QY      41 ProGluYsaArgLeuGIuLeuValAlaAlaIleAsnSerAspGIyGIyIleThrTYrTYr 60
      |||
      121 CCAGAGAAGAGGCTGAGATTGTCGACGCAATTAATCAATGGTGGTTTCACCTACTAT 180
QY      61 LeuAspThrValIyGIyArgPheThrIleSerArgAspAsnAlaIyAsnThrLeuTYr 80
      |||
      181 CCAGACACTGTGAAGGCCGATTCACCATTCACAGAGCAATGCCAAGAACACCTGTAC 240
QY      81 LeuGlnMetSerSerLeuIySerGIuAspThrAlaLeuPheTYrCysAlaArgHisArg 100
      |||
      241 CTGCAATGAGCACTGGAAGTCTGAGAGACACGGCCTTCTACTATTGTGCAAGACCGAG 300
QY      101 -----SerGIyTYrPheSer--MetAspTYrTrpGIyGlnGIyThrSerValThrVal 117
      |||
      301 TTGATACTTCTCTACGAGACCTGGTTTGCTTACTGGGGCCAAAGGAGACTGTGTCACGTGC 360
QY      118 SerSer 119
      |||
      361 TCTGCA 366
Db
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Search completed: June 3, 2006, 04:13:01
Job time : 395.447 secs

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 3, 2006, 04:13:15 ; Search time 2998.94 Seconds
(without alignments)

3328.373 Million cell updates/sec

Title: US-10-635-908-6

Sequence: 1 DVKLVESSGGGLVKGSLKLT.....RSGYFMDYGGQTSVTYSS 119

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-OUTFMT=pro -NOR=exc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h
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-WAMP TIMOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
7: gb_est8.*
8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_gsa1.*
12: gb_gsa2.*
13: gb_gsa3.*
14: gb_gsa4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495.5	80.3	861	2	BI455668 603173862
2	495	80.2	603	3	BQ266309
3	494	80.1	650	7	BF579001 602096117
4	482	78.1	774	7	BF581450 602100853

5	478.5	77.6	837	2	BQ66335
6	468.5	75.9	987	7	BF577496
7	466	75.5	689	7	BF579926
8	465.5	75.4	823	1	AA170256
9	456	73.9	662	7	BF163874
10	455	73.7	662	7	BF142302
11	454.5	73.7	562	9	DA975437
12	453.5	73.5	553	9	DA976755
13	453.5	73.5	584	9	DA972115
14	453.5	73.5	667	4	BY750520
15	453.5	73.5	1565	6	AK156019
16	452.5	73.3	552	9	DA982966
17	451	73.1	901	3	BUS23851
18	450.5	73.0	562	9	DA980210
19	450	72.9	913	7	BF162056
20	449	72.8	557	9	DA972534
21	449	72.8	559	9	DA979611
22	449	72.8	560	9	DA987096
23	449	72.8	573	9	DA980582
24	448.5	72.7	777	5	CK476776
25	447.5	72.5	469	1	AI645111
26	447	72.4	498	9	DA971158
27	446.5	72.4	546	9	DA947087
28	446	72.3	969	7	BF579260
29	445.5	72.2	504	9	DA977056
30	445.5	72.2	580	9	DA988280
31	445.5	72.2	1586	6	BC018461
32	445	72.1	550	9	DA976042
33	445	72.1	579	9	DA974187
34	444.5	72.0	593	9	DB190243
35	444	72.0	550	9	DA975094
36	444	72.0	875	3	BQ706723
37	444	72.0	968	3	BQ706746
38	443	71.8	545	9	DB102282
39	443	71.8	561	9	DA983749
40	442.5	71.7	572	9	DA954615
41	442.5	71.7	572	9	DA981934
42	442	71.6	578	9	DA820045
43	442	71.6	908	7	BF161883
44	441.5	71.6	515	4	CA571547
45	441.5	71.6	542	9	DA971342

ALIGNMENTS

RESULT 1
BI455668
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI455668 861 bp mRNA linear EST 21-AUG-2001
603173862F1 NCT_CGAP_Mams Mus musculus cDNA clone IMAGE:5253279 5',
mRNA sequence.
BI455668
BI455668.1 GI:15246324
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 861)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straube, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LLM1639 row: 1 column: 16
High quality sequence stop: 780.

FEATURES
source

Location/Qualifiers
1. 861
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5253279"
/issue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_11b="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt; Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

ORIGIN

Alignment Scores:

Pred. No.: 2.5e-55 Length: 861
Score: 495.50 Matches: 97
Percent Similarity: 89.9% Conservative: 10
Best Local Similarity: 81.5% Mismatches: 11
Query Match: 80.3% Indels: 1
DB: 2 Gaps: 1

US-10-635-908-6 (1-119) x B1455668 (1-861)

QY 1 AapVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuValLeu 20
:::|||||
DB 128 GAAGTGAAGCTGGTGGAGCTGGGGGAGGCTTAGTCCAGCTGGAGGCTCCCTGAATC 187
QY 21 SerCyAlAlSerGlyPheThrPheSerAenTyTyMetSerTrpValArgGlnTr 40
188 TCTGTGCAACCTCTGGATTCACTTCACTGACTATTACATTGAGGTTGCCAGACT 247
QY 41 ProGluValArgLeuGluIleuValAlaAlaIleAenSerAspGlyGlyIleThrTyTy 60
248 CAGAGAAAGAGCTGGAGTGGCTGCATCAATTAGTAATGGTGGTGGTGCACCTATTAT 307
QY 61 LeuAspThrVallyGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTy 80
DB 308 CAGACACTGTAAAGGCCGATTCACCATCTCCAGAGACAAATGCCAAGAACCCCTGTAC 367
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyTyCyAlAlaArgHisArg 100
DB 368 CTGCAAAATAGACGCTGTGAAGTCTGAGACACAGCCATGATTATTCGTCCAAAGA--ACT 424
QY 101 SerGlyTyPheSerMetAspTyTyTrpGlyGlnGlyThrSerValThrValSerSer 119
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DB 425 AACTGTAATGCTATGCTATGCACTACTGGGATCAAGAACTCACTCACTCTCTCTCA 481

RESULT 2
BQ266309 603 bp mRNA linear EST 07-MAY-2002
LOCUS BQ266309.1 NCI CGAP Mam5 Mus musculus cDNA clone IMAGE:2865417
DEFINITION 5' mRNA sequence.
ACCESSION BQ266309.1 GI:20491374
VERSION BQ266309.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen/Robin Humphreys

FEATURES
source

cDNA Library Preparation: Life Technologies
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
MGI:1046189
Plate: L1AM7069 row: F column: 10
Seq primer: M13p1 reverse primer (ABI).

Location/Qualifiers

1. 603
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:2865417"
/issue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_11b="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt; Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

ORIGIN

Alignment Scores:

Pred. No.: 1.75e-55 Length: 603
Score: 495.00 Matches: 96
Percent Similarity: 91.6% Conservative: 13
Best Local Similarity: 80.7% Mismatches: 8
Query Match: 80.2% Indels: 2
DB: 3 Gaps: 1

US-10-635-908-6 (1-119) x BQ266309 (1-603)

QY 1 AapVallyLeuValGluSerGlyGlyLeuVallyLeuGlyGlySerLeuValLeu 20
:::|||||
DB 132 GAGGTGCACCTGGTGAAGCTGGGGGAGGCTTAGGAAGCTGGTGGGCTCCCTGAATC 191
QY 21 SerCyAlAlSerGlyPheThrPheSerAenTyTyMetSerTrpValArgGlnTr 40
DB 192 TCTGTGCAACCTCTGGATTCACTTCACTGACTATTAGGCAATGCTTGGTCCAGACT 251
QY 41 ProGluValArgLeuGluIleuValAlaAlaIleAenSerAspGlyGlyIleThrTyTy 60
DB 252 CCGAAGAAAGAGCTGGAGTGGCTCCAGACATTAATCAATGCTGTACCAACCCACTAT 311
QY 61 LeuAspThrVallyGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTy 80
DB 312 CAGACACTGTAAAGGCCGATTCACCATCTCCAGAGACAAATGCCAAGAACCCCTGTAC 371
QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyTyCyAlAlaArgHisArg 100
DB 372 CTGCAAAATAGACGCTGTGAAGTCTGAGACACAGCCCTGATTATTCAGTTCAACATGCT 431
QY 101 SerGlyTyPheSerMetAspTyTyTrpGlyGlnGlyThrSerValThrValSerSer 119
:::|||||
DB 432 AACTTCTACTTT-----GACTACTGGGGCCAAAGCACCACTCTCACTCTCTCA 482

RESULT 3
BF579001 650 bp mRNA linear EST 12-DEC-2000
LOCUS BF579001 602096117F1 NCI CGAP Co24 Mus musculus cDNA clone IMAGE:4215844 5'
DEFINITION mRNA sequence.
ACCESSION BF579001
VERSION BF579001.1 GI:11652713
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia: Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 650)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM9792 row: b column: 05
High quality sequence stop: 649.
Location/Qualifiers

FEATURES

source

1. 650
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4215844"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:

Pred. No.:	2,666-55	Length:	650
Score:	494.00	Matches:	102
Percent Similarity:	90.0%	Conservative:	6
Best Local Similarity:	85.0%	Mismatches:	7
Query Match:	80.1%	Indels:	5
DB:	7	Gaps:	1

US-10-635-908-6 (1-119) x BF579001 (1-650)

QY 1 AspVallysluValgluSerGlyGlyLeuVallysluGlyGlySerLeuYslu 20
128 GAGGTGACGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCTGAGGCTCCCTGAACTC 187
DB 188 TCCGTGACAGCTCTGATTCACTTCAGTAACATGACATGCTTGGGTCGCGCAACT 247
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyRTyrMetSerTPValArgGlnThr 40
188 TCCGTGACAGCTCTGATTCACTTCAGTAACATGACATGCTTGGGTCGCGCAACT 247
QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
248 CCGAGAGAGAGGCTGGAGTGGTGCAGCCATTAAATGATGATGATGATGATGATGAT 307
DB 308 CCAGACACTGTAAGGCGCATTCACCATCTCCAGAGCAATGCGCAAGAACACCTGTAT 367
QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlaYsAsnThrLeuTyr 80
308 CCAGACACTGTAAGGCGCATTCACCATCTCCAGAGCAATGCGCAAGAACACCTGTAT 367
QY 81 LeuGlnMetSerSerLeuYsSerGluAspThrAlaLeuPheTyrCyS-AlaArgHisArg 100
368 CTGACATGACAGCTGAGGTCTGAGAGACACACCTTGTATTACTGGTGCAGAACAT- 425
DB 100 gSerGlyTyrPheSerMetAspTyRTyrGlyGlnGlyThrSerValThrValSerSer 119
426 -----CTGACTATGACTACTGGGGTCAAGAACCTCACTCACTCTCTCA 473

RESULT 4
BF581450 774 bp mRNA linear EST 12-DEC-2000
LOCUS 602100853p1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4224109 5',
DEFINITION mRNA sequence.
ACCESSION BF581450
VERSION BF581450.1 GI:11655162

KEYWORDS

EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM9813 row: j column: 14
High quality sequence stop: 675.
Location/Qualifiers

FEATURES

source

1. 774
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4224109"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:

Pred. No.:	1,396-53	Length:	774
Score:	482.00	Matches:	96
Percent Similarity:	84.8%	Conservative:	10
Best Local Similarity:	76.8%	Mismatches:	13
Query Match:	78.1%	Indels:	6
DB:	7	Gaps:	1

US-10-635-908-6 (1-119) x BF581450 (1-774)

QY 1 AspVallysluValgluSerGlyGlyLeuVallysluGlyGlySerLeuYslu 20
118 GAGGTGACGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCTGAGGCTCCCTGAACTC 177
DB 178 TCCGTGACAGCTCTGATTCACTTCAGTAAGCTAAGCATGCTTGGGTCGCGCAACT 237
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyRTyrMetSerTPValArgGlnThr 40
178 TCCGTGACAGCTCTGATTCACTTCAGTAAGCTAAGCATGCTTGGGTCGCGCAACT 237
QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
238 CCGAGAGAGAGGCTGGAGTGGTGCAGCCATTAAATGATGATGATGATGATGATGAT 297
DB 238 CCAGACACTGTAAGGCGCATTCACCATCTCCAGAGCAATGCGCAAGAACACCTGTAT 357
QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlaYsAsnThrLeuTyr 80
298 CTAGACCTGTAAGGCGCATTCACCATCTCCAGAGCAATGCGCAAGAACACCTGTAT 357
QY 81 LeuGlnMetSerSerLeuYsSerGluAspThrAlaLeuPheTyrCyS-AlaArgHisArg 100
358 CTGCAATGACAGCTGAGGTCTGAGAGACACACCTTGTATTACTGGTGCAGAACATGG 417
DB 101 -----SerGlyTyrPheSerMetAspTyRTyrGlyGlnGlyThrSerValThrValSerSer 114
418 GATATATATGCTACTATTAAGAGACGACTACTTGTGACTTATGGGCCAAGGACCACT 477
QY 115 ValThrValSerSer 119
478 CTCACAGTCTCTCTCA 492

RESULT 5
BG966355 837 bp mRNA linear EST 12-JUN-2001
LOCUS 602832843f1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4987379 5',
DEFINITION mRNA sequence.
ACCESSION BG966355
VERSION BG966355.1 GI:14353392
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 837)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10998 row: e column: 12
High quality sequence stop: 692.
Location/Qualifiers
1..837
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4987379"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NciI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Alignment Scores:
Pred. No.: 4,59e-53 Length: 837
Score: 478.50 Matches: 96
Percent Similarity: 86.7% Conservative: 8
Best Local Similarity: 80.0% Mismatches: 15
Query Match: 77.6% Indels: 1
DB: 2 Gaps: 1
US-10-635-908-6 (1-119) x BG966355 (1-837)
QY 1 AapvallyleuValGluSerGlyGlyLeuVallyleuGlySerleuValleu 20
Db 135 GAAGTATGCTGCTGGAGCTGCGGAGGCTTGTGAAGCCTGAGAGGCTCCGAAACTC 194
QY 21 SerCyAlAlAlAserylYpethrPheserAntYrTyMeSerTrpValArgIntnr 40
Db 195 TCCTGTGACGCTCTGATTCACCTTCAGTATACCATGCTTGCGTCCGACAGCT 254
QY 41 ProGluValArgLeuGluLeuValAlAlAlAlAsnSerAspGlyGlyIleThrYrYr 60
Db 255 CCGGCGAAGAGGCTGAGTGGGTCGCAACCATTAAGTGGTGGTAAACACTACTAT 314
QY 61 LeuAspThrVallyleGlyArgpethrIleSerArxAspAsnAlAlAsnThrLeuYr 80
Db 315 CCGAAGAAATATGAGGCGGATTCACCATTCAGAGACATCCAGAAACCTCTATC 374
QY 81 LeuGluMetSerSerleuYrSerGlyAspThrAlAlAlAlAlAlAlArgH1sArg 100
Db 375 CTCGAATATGAGCTGAGGCTGAGAGACACGGCTTGTATTAAGTGTGACAGCGGTT 434

QY 101 SerGly---TyrPheserMetAspYrTrpGlyGlnGlyThrSerValThrValSerSer 119
Db 435 TATGTAACCTCTATGATGATGATGAGGCTCAAGAACTCATGACCGCTCTCTCA 494
RESULT 6
BF577496 987 bp mRNA linear EST 12-DEC-2000
LOCUS 602092343f1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4206707 5',
DEFINITION mRNA sequence.
ACCESSION BF577496
VERSION BF577496.1 GI:11651208
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 987)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9768 row: e column: 12
High quality sequence start: 3
High quality sequence stop: 699.
Location/Qualifiers
1..987
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4206707"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NciI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Alignment Scores:
Pred. No.: 1,28e-51 Length: 987
Score: 468.50 Matches: 93
Percent Similarity: 85.0% Conservative: 9
Best Local Similarity: 77.5% Mismatches: 17
Query Match: 75.9% Indels: 1
DB: 7 Gaps: 1
US-10-635-908-6 (1-119) x BF577496 (1-987)
QY 1 AapvallyleuValGluSerGlyGlyLeuVallyleuGlySerleuValleu 20
Db 107 GATGTGACCTGCTGAGTCTGGGAGGCTTGTGACCTGAGAGGCTCCGAAACTC 166
QY 21 SerCyAlAlAlAserylYpethrPheserAntYrTyMeSerTrpValArgIntnr 40
Db 167 TCCTGTGACGCTCTGATTCACCTTCAGTATGAGTGAATGACTGGTTCGTCAAGCT 226
QY 41 ProGluValArgLeuGluLeuValAlAlAlAlAlAlAlAsnSerAspGlyGlyIleThrYrYr 60
Db 227 CCGAAGAAAGGCTGAGTGGGTCGCAATATTTGTAAGCATGCTGATCCATCTAT 286
QY 61 LeuAspThrVallyleGlyArgpethrIleSerArxAspAsnAlAlAsnThrLeuYr 80

Db 287 GCAGACACAGTGAAGGCGCATTCACACATCTCCAGACATGCCAAGAACCCCTGCTC 346
Qy 81 LeuGlnMetSerSerLeuYssSerGlyuAspThrAlaLeuPheTyrCysAlaArgHisArg 100
Db 347 CTGCACATATGACCGATCTTAAGGTTGAGACACGCGCATGATTAATCTGTGCAACACCTAT 406
Qy 101 SerGly---TyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 119
Db 407 AGTAACCATTAATCTTCTGTAATGACTACTGGGTCAGAGAACTCAGTCAACCTCTCTCTCA 466
RESULT 7
BF579926 689 bp mRNA linear EST 12-DEC-2000
LOCUS 602095194F1_NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4209551 5',
DEFINITION mRNA sequence.
ACCESSION BF579926 GI:11653638
VERSION BF579926.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 689)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM9775 row: k column: 24
High quality sequence stop: 685.
Location/Qualifiers
1..689
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4209551"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NCI_CGAP_Co24"
/note="Organ: Colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."
ORIGIN
Alignment Scores:
Pred. No.: 1.66e-51 Length: 689
Score: 466.00 Matches: 96
Percent Similarity: 88.3% Conservative: 10
Best Local Similarity: 80.0% Mismatches: 9
Query Match: 75.5% Indels: 5
Gaps: 2
US-10-635-908-6 (1-119) x BF579926 (1-689)
Qy 1 AspyValysLeuValGlySerGlyGlyValysLeuGlyValSerLeuYssLeu 20
Db 131 GAGGTGCGCTGGTGGAGCTCTGGGGAGCTTAAGTAAGCCTGGAGGATCCCTGAAGATC 190
Qy 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
Db 191 TCTGTGTGAGGCTCTGATTCACCTTCACTGACATGACATGCAATGCTTGGGTTCCGACAGT 250
Qy 41 ProGlnYsaTgLeuGlnLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60

Db 251 CCGAGAAAGAGCTGAGAGTGGGTCGACCATTAATTAATGATGTGTAATACCTACTAT 310
Qy 61 LeuAspThrValIleGlyValArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTyr 80
Db 311 TCAGACACTATGAAGGCGCATTCACCATCTCAGAGACAATGCCAAGACACCTGTAT 370
Qy 81 LeuGlnMetSerSerLeuYssSerGlyuAspThrAla-LeuPheTyrCysAlaArgHisArg 100
Db 371 CTGCACATATGACGATCTTAAGGTTGAGACACGCGCTTAATTAATTAATGCTA-----AG 424
Qy 100 gSerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 119
Db 425 AGGGGGTACTTC-----GATCTCTGGGGCGAGGAGCGCGGTCAACGTCCTCTCA 476
RESULT 8
AA170256 823 bp mRNA linear EST 16-FEB-1997
LOCUS AA170256
DEFINITION m87g10.r1 Soares mouse 3nbms Mus musculus cDNA clone IMAGE:618594
5' similar to gb:U00821 IG HEAVY CHAIN PRECURSOR V-III REGION
(HUMAN); gb:U00821 Mouse mRNA fragment for immunoglobulin mu
encoding the C-terminus (MOUSE);, mRNA sequence.
ACCESSION AA170256 GI:1748794
VERSION AA170256
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 823)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacey, M., Le, M., Martin, J., Morris, M.,
Schellenger, K., Stepcoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:379418
Putative full length read
vector to vector length is 867
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 492.
Location/Qualifiers
1..823
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:618594"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_id="Soares mouse 3nbms"
/note="Vector: pT73D-PacI; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACCAATCTGAAGTGGAGCGCGCGCTGTTTTTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:	2,496-51	Length:	823
Score:	465.50	Matches:	93
Percent Similarity:	84.4%	Conservative:	10
Best Local Similarity:	76.2%	Mismatches:	16
Query Match:	75.4%	Indels:	3
DB:	1	Gaps:	1

US-10-635-908-6 (1-119) x AA170256 (1-823)

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QY 1 AapValLyLeuValGluSerGlyGlyLeuValLyLeuGlyGlySerLeuValLeu 20
DB 118 GAGGTGACCTGAGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 177
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAenTyTyMetSerTyPalaArgGlnTr 40
DB 178 TCCTGTGACGCTTGAGATTCACTTCACTAGCTATGCCATGTCTGGGTGCCAGACT 237
QY 41 ProGluLyArgLeuGluLeuValAlaAlaLeuSerAaspGlyGlyIleThrTyTy 60
DB 238 CCAGAGAGAGAGGCTGAGGTGGATTCATTAAGTATGATTAATTAATTAATTAAT 297
QY 61 LeuAapThrValLyLeuGlyPheThrIleSerAaspAenAlaLyAenThrLeuTy 80
DB 298 GCAGACACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357
QY 81 LeuGlnMetSerSerLeuLySerGlyAapThrAlaLeuPheTyCyAlaArg----- 98
DB 358 CTGCAAAATGACAGCTGAGAGTGTGAGACACAGCAGCATATTAATTAATTAATTAAT 417
QY 99 ---HlaArgSerGlyTyPheSerMetAapTyTyTPGlyGlnGlyThrSerValThrVal 117
DB 418 CTCTGTGTAAGTGGTCTACTACTTGTGACTACTGGGCAAGGACCACTCTCACAGTC 477
QY 118 SerSer 119
DB 478 TCCTCA 483
RESULT 9
BF163874 662 bp mRNA linear EST 30-OCT-2000
LOCUS B163874 NC1 CGAP Lu29 Mus musculus cDNA clone IMAGE:3991460 5'
DEFINITION mRNA sequence.
ACCESSION B163874.1 GI:11044152
VERSION B163874
KEYWORDS Mus musculus (house mouse)
SOURCE EST.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclerogamathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 662)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Plate: L1AM9204 row: 1 column: 21
High quality sequence stop: 658.
Location/Qualifiers
1..662
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
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ORIGIN

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/db_xref="taxon:10090"
/clone="IMAGE:3991460"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: Lung; Vector: pCMV-SPORT6; Site: 1: SalI;
Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
```

Alignment Scores:

Pred. No.:	3,446-50	Length:	662
Score:	466.00	Matches:	96
Percent Similarity:	86.8%	Conservative:	9
Best Local Similarity:	79.3%	Mismatches:	12
Query Match:	73.9%	Indels:	4
DB:	7	Gaps:	3

US-10-635-908-6 (1-119) x BF163874 (1-662)

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QY 1 AapValLyLeuValGluSerGlyGlyLeuValLyLeuGlyGlySerLeuValLeu 20
DB 123 GAGGTGACCTGAGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 182
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAenTyTyMetSerTyPalaArgGlnTr 40
DB 183 TCCTGTGACGCTTGAGATTCACTTCACTAGCTATGCCATGTCTGGGTGCCAGACT 242
QY 41 ProGluLyArgLeuGluLeuValAlaAlaLeuSerAaspGlyGlyIleThrTyTy 60
DB 243 CCAGAGAGAGGCTGAGGTGGATTCATTAAGTATGATTAATTAATTAATTAATTAAT 299
QY 61 LeuAapThrValLyLeuGlyPheThrIleSerAaspAenAlaLyAenThrLeuTy 80
DB 300 CCAGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 359
QY 81 LeuGlnMetSerSerLeuLySerGlyAapThrAlaLeuPheTyCyAlaArgHlaArg 100
DB 360 CTCCAAAATGACAGCTGAGAGTGTGAGACACAGCAGCATATTAATTAATTAATTAAT 416
QY 101 SerGlyTyPheSer-----MetAapTyTyTPGlyGlnGlyThrSerValThrValSer 118
DB 417 GGTGTACTTACGAGATGATTCATTCATGTCTGGGCGCAGGAGCACAGGTCACCGTCTC 476
QY 119 Ser 119
DB 477 TCA 479
RESULT 10
BF142302 1012 bp mRNA linear EST 24-OCT-2000
LOCUS B142302
DEFINITION 60179184F1 NC1 CGAP Lu30 Mus musculus cDNA clone IMAGE:4022459 5'
RNA sequence.
ACCESSION B142302
VERSION B142302
KEYWORDS B142302.1 GI:10981252
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclerogamathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 1012)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

http://image.jnl.gov
Plate: LHAM9279 row: h column: 12
High quality sequence stop: 711.

FEATURES

source

1. 1012
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech 11"
/db_xref="taxon:10090"
/clone_xref="IMAGE:4022459"
/issue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_1ib="NCI-CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; transgenic model MMT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Alignment Scores:

Pred. No.: 8,58e-50 Length: 1012
Score: 455.00 Matches: 91
Percent Similarity: 84.0% Conservative: 9
Best Local Similarity: 76.5% Mismatches: 17
Query Match: 73.7% Indels: 2
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x BFL42302 (1-1012)

QY 1 AspvAllyleuValguSerGlyGlyLeuVallyleuGlySerLeuValleu 20
DB 101 GAGGTGAGCTGGTGGAGCTGGGGAGGCTTACTGAAAGCTGAGAGGCTCCGAAACTC 160
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrtMetSerTPValArgInThr 40
DB 161 TCCTGTGACCCCTGTGATTCACCTTCAGTGACATGGAATGCACTGGTTCGACAGCT 220
QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyIleThrTyrt 60
DB 221 CCAGAGAAAGGGCTGAGTGGGTGCATACATAGTGGCAGTACATACATCTACTAT 280
QY 61 LeuAspThrVallysglyArgPheThrIleSerArgAspAsnAlaValAsnThrLeu 80
DB 281 GCAGACACAGTGAAGGGCCGATTCACATCCAGAGCAATGCAAGAACACCTGTC 340
QY 81 LeuGlnMetSerSerLeuYsSerGlyAspThrAlaLeuPheTyrtCyAlaArgHisArg 100
DB 341 CTGCAAAATGACCACTTAAGGTCTGAGACACGGCCATGTATCTGTGCA-----AGC 394
QY 101 SerGlyTyrtPheSerMetAspTyrtTyrtGlyGlnGlyThrSerValThrValSerSer 119
DB 395 CCAAGTTACTCCCTATGACTACTGAGGAGTCAAGAACTCAGTACCGTCTCTCA 451
RESULT 11
DA975437 562 bp mRNA linear EST 13-NOV-2005
LOCUS DA975437 SYN0V2 Homo sapiens cDNA clone SYN0V2005900 5', mRNA
DEFINITION sequence.
DA975437
ACCESSION DA975437 GI:82346288
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 562)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Teurillem,H., Wakiyuri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kishida,N.,

TITLE

JOURNAL

PUBMED

COMMENT

Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi,Fuji,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T., and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction;
Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing; RAB.

FEATURES

source

1. 562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_xref="SYNOV2005900"
/issue_type="synovial membrane tissue from rheumatoid
arthritis"
/clone_1ib="SYNOV2"
/note="Vector: pME18SFL3"

ORIGIN

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Pred. No.: 4,33e-50 Length: 562
Score: 454.50 Matches: 88
Percent Similarity: 86.4% Conservative: 14
Best Local Similarity: 74.6% Mismatches: 15
Query Match: 73.7% Indels: 1
DB: 9 Gaps: 1

US-10-635-908-6 (1-119) x DA975437 (1-562)

QY 2 VallyleuValguSerGlyGlyLeuVallyleuGlySerLeuValleuSer 21
DB 142 GTGAGCTGGTGGAGTCTGGGGAGGCTGTGATCAAGGCTGAGGCTCCAGACTCC 201
QY 22 CyAlaAlaSerGlyPheThrPheSerAsnTyrtMetSerTPValArgInThrPro 41
DB 202 TGTGCACCCCTGTGATTCACCTTCAGTACTACATGAGCTGATCCGACAGCTCA 261
QY 42 GluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyIleThrTyrt 61
DB 262 GCGAAGGGCTGAGTGGGTTCATACATAGTACTGTAGACATATCAAGCA 321
QY 62 AspThrVallysglyArgPheThrIleSerArgAspAsnAlaValAsnThrLeu 81
DB 322 GACTCTGGAAGGGCCGATTCACCATCTCCAGGAGCAACGCAAGAACTCATCTG 381
QY 82 GlnMetSerSerLeuYsSerGlyAspThrAlaLeuPheTyrtCyAlaArgHisArgSer 101
DB 382 CAAATGAAACAGCCCTGAAGCCGAGAGACACGGCCGTGTATTACTGTGAGAGCAAGAGAT 441
QY 102 GlYTyrtPheSerMetAspTyrtTyrtGlyGlnGlyThrSerValThrValSerSer 119
DB 442 GGCTAT---AAGTTGACTACTGGGCGAGGAACCTGTGACCGTCTCTCA 492
RESULT 12
DA976755 553 bp mRNA linear EST 13-NOV-2005
LOCUS DA976755 SYN0V2 Homo sapiens cDNA clone SYN0V200540 5', mRNA
DEFINITION sequence.
DA976755
ACCESSION DA976755

VERSION	DA976755.1	GI:82369866
KEYWORDS	EST	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	
AUTHORS	1 (bases 1 to 553) Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Teurittani,K., Makaguri,H., Iehi,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Ioneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Nagatsuma,M., Murakawa,K., Ishida,S., Iishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.	
TITLE	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes	
JOURNAL	Genome Res. 16 (1), 55-65 (2006)	
PUBMED	16344560	
COMMENT	Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdna@nifty.com NBD human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation, 3'-end one pass sequencing: RAB.	
FEATURES	Location/Qualifiers	
source	1..553 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="SYNOV2007540" /cruise_type="synovial membrane tissue from rheumatoid arthritis" /clone_1ib="SYNOV2" /note="Vector: pME18SFL3"	
ORIGIN		
Alignment Scores:		
Pred. No.:	5,766-50	553
Score:	453.50	88
Percent Similarity:	83.7%	Conservative: 15
Best Local Similarity:	71.5%	Mismatches: 15
Query Match:	73.5%	Indels: 5
DB:	9	Gaps: 1
US-10-635-908-6 (1-119) x DA976755 (1-553)		
Qy	2 VallyLeuValGluSerGlyGlyLeuValIlyLeuGlyGlySerLeuIySerLeuSer 21	
Db	141 GTCGACGCTGTGAGCTCGGGGAGGCTTGTCGACGAGCCGCGAGGGTCCCTAGACTCTCC 200	
Qy	22 CyAlaAlaIseGlyPheThrPheSerAenIyTyrmSetTTPValArgInThrPro 41	
Db	201 TGTGCGCCTCTGAGATTCACCTTCAGTGACTCTCATGACTGAGTCGCGCAGGCTCCA 260	
Qy	42 GluVArArgLeuGluLeuValAlaAlaIleAenSerAapGlyGlyIleThrTyTyrrLeu 61	
Db	261 GGGAAAGGGCTGGAGTGGGATTCATCATCTAGTAGTGGTAATACCATATACACGA 320	
Qy	62 AapThrValIyGclYArgPheThrIleSerArGAspAenAlIyAsnThrDeuTyrrLeu 81	
Db	321 GACTGTGTAAGGGCCGATTCAACATCTCAAGGACCAACGCGCAAGACTCATGTATCTG 380	
Qy	82 GlnMetSerSerLeuIySerGluAapThrAlaLeuPheTyCyAlaArgHIsArgSer 101	
Db	381 CAAATTAACAGCCTTGAGCCGAGGACGAGCGGCCCTGTATTATCTGTGCGAGACTCACCGGT 440	

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Oy      102 G|Y-----TYPHSEMMeAspTYrTpGlyGInGlyTYRSeValThr 116
Db      441 GGTCACCTCTACTACTACTACTACTACAGATGGAGGTCTGGGGCCAAAGGACCAAGCAGTACC 500

RESULT 13
Oy      117 ValSerSer 119
Db      501 GTCTCCTCA 509

LOCUS   DA972115
DEFINITION DA972115 SYN0V2 Homo sapiens cDNA clone SYN0V2001766 5', mRNA
sequence.
ACCESSION DA972115
VERSION   DA972115
KEYWORDS  DA972115.1 GI:82114937
SOURCE    EST.
ORGANISM  Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 584)
Kimura,K., Wakamatsu,A., Suzuki,Y., Oca,T., Nishikawa,T.,
Yamaashita,R., Yamamoto,J., Sekine,M., Tauritani,K., Wakeguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kuehlde,N.,
Yonekawa,T., Otuka,R., Kaneda,K., Yokoi,T., Kondo,H., Wagatsuna,M.,
Murakawa,K., Ishida,S., Ishihashi,T., Takahashi-Fujii,A.,
Tanase,T., Negai,K., Kikuchi,H., Nakai,K., Inogai,T. and Sugano,S.
Diversification of transcriptional modulation: Large-scale
identification and characterization of putative alternative
promoters of Human Genes
Promoter Res. 16 (1), 55-65 (2006)
16344560
JOURNAL   Contact: Takao Inogai
PUBMED    FUD Project (HRI Team)
COMMENT    Helix Research Institute
           2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
           Tel.: 81-438-52-3975
           Fax: 81-438-52-3986
           Email: fjd-chna@infocity.com
           NEO human cDNA project (New Energy and Industrial Technology
           Developmental Organization, Japan); cDNA library construction:
           Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
           Research Association for Biotechnology (RA) and Biotechnology
           Center, National Institute of Technology and Evaluation; 3'-end one
           pass sequencing: RA).
FEATURES             Location/Qualifiers
     source            1..584
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="SYNOV2001766"
                     /tissue-type="synovial membrane tissue from rheumatoid
                     arthritis"
                     /clone_id="SYNOV2"
                     /note="Vector: pME18SF3"

ORIGIN
Alignment Scores:
Pred. No.:          6,23e-50              Length:          584
Score:              453.50                Matches:           87
Percent Similarity: 83.7%                 Conservative:       16
Best Local Similarity: 70.7%               Mismatches:        15
Query Match:        73.5%                  Indels:            5
DB:                 9                      Gaps:              1
US-10-635-908-6 (1-119) x DA972115 (1-584)

Oy      2 VallysLeuValGlusErGIyGlyLeuValylsLeuGlySerLeuLysLeuSer 21
Db      141 GTGCAGCGTGGAAGTCTGGGGGAGGCGCTTGGTCAAGCCTGGAGGGGTCCCTAAGACTTCC 200

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OY 22 CysAlaAspSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThrPro 41
DB 201 TGTGACGCTCTGAGTTCCTTCACTACTGACTCTACATAGCTGATCCGACGGCTCA 260
OY 42 GtUlyArGleuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyrLeu 61
DB 261 GGGAAAGGGGCTGAGAGGGTTTCATTCATTAGTAGAGGTAGTACCATATATACACGA 320
OY 62 AApTValIleGlyIleArGpHeThrIleSerArgAspAsnAlaIleAsnThrIleu 81
DB 321 GACTCTGTAAAGGGCGGATTCACCATCTCCAGGACCAAGCCAGAACCTCAGTATCTG 380
OY 82 GlnMetSerSerLeuIleuSerGluAspThrAlaLeuPheTyrCysAlaArgHisArgSer 101
DB 381 CAAATGAACACGCTAGACCCAGACGACGCGCTATATACGTGCGAGATACCGGGCT 440
OY 102 Gly-----TyrPheSerMetAspTyrTyrGlyGlnGlyThrSerValThr 116
DB 441 GGTAACTCCTACTACTACTACTACGTATGACGTCTGGGGCCAGAGGACCAAGGTACAC 500
OY 117 ValSerSer 119
DB 501 GTCTCTCTCA 509

RESULT 14
BY750520 667 bp mRNA linear EST 17-DBC-2002
LOCUS BY750520 RIKEN full-length enriched, activated spleen Mus musculus
DEFINITION CDNA clone F830004G20 5', mRNA sequence.
ACCESSION BY750520
VERSION BY750520.1 GI:27180458
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Ose, N., Saito, R., Suzuki, H., Yamana, K.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bull, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batilov, S., Beisel, K. W., Blake, J. A., Brad, D., Bruscia, V.,
Chochia, C., Corbani, L. E., Cousins, S., Dalla, E., Drganci, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pettes, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Sempole, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
Weil, C., Wilming, L. G., Wynshaw-Boris, A., Yamagata, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayasue, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Aikawa, T., Fukuda, S., Hara, A., Hashizume, M., Imclani, D., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
JOURNAL PUBMED
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

```

```

1-7-22 Suehico-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-ree@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P.,
Fukuda, S., Hashizume, M., Hayashida, K., Hirozane, T., Hori, F.,
Imokani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC Building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
source Location/Qualifiers
1.667
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830004G20"
/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN
Alignment Scores:
Pred. No.: 7.53e-50 Length: 667
Score: 453.50 Matches: 91
Percent Similarity: 83.2% Conservative: 8
Best Local Similarity: 76.5% Mismatches: 19
Query Match: 73.5% Indels: 1
DB: 4 Gaps: 1
US-10-635-908-6 (1-119) x BY750520 (1-667)
OY 1 AspValIleLeuValAlaIleAsnSerAspGlyGlyIleThrTyrTyrLeu 20
DB 131 GAAGTCACAGCTGTGAGTCTGGGAGGAGCTTAGTGAAGCTGAGAGGCTCCGAAATC 190
OY 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
DB 191 TCTGTGACGCTCTGAGTTCCTTCACTACTGACTCTACATAGCTGATCCGACGGCTCA 250
OY 41 ProGluIleArGleuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
DB 251 CCGAAAGGGGCTGAGAGGGTTTCATTCATTAGTAGAGGTAGTACCATATATACACGA 310
OY 61 LeuAspThrValIleGlyIleArGpHeThrIleSerArgAspAsnAlaIleAsnThrIleu 80
DB 311 CCAGACAAATGATAAGGGCGGATTCACCATCTCCAGGACCAAGCTCAGTATCTG 370
OY 81 LeuGlnMetSerSerLeuIleuSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100

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Db	371	CTGCAAAATGACCCATCTGAAGTCGTAGAGACACAGCCATGTAATTACTGTGCAAGAGAT----	427
Qy	101	SerGlyTyrPheSerMetLeuTyrTrpGlyGlnGlyThrSerValThValSerSer 119	
Db	428	GGGGGATTACGACAGAGTTGCTTACTGGGGCCAGAGAGACTCTGGTCACTGTCTCTGCA 484	
RESULT 15			
AK156019			
LOCUS			
DEFINITION		Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:FB30004G20 product:immunoglobulin heavy chain 4 (aermun IgG1), full insert sequence.	
ACCESSION		AK156019	
VERSION		AK156019.1 GI:74217594	
KEYWORDS		HTC; CAP trapper.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.	
AUTHORS		Carninci, P. and Hayashizaki, Y.	
TITLE		High-efficiency full-length cDNA cloning	
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)	
PUBMED		10394636	
REFERENCE			
AUTHORS		2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
TITLE		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)	
PUBMED		11042159	
REFERENCE			
AUTHORS		3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, N., Nishie, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawaji, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
TITLE		RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)	
PUBMED		11076861	
REFERENCE			
AUTHORS		4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, Y., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kaenkawa, T., Saito, R., Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuell, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bul, C., G. Fleischer, C., Fujita, M., Gariboldi, M., Gattilino, S., Hill, D., Hofmann, M., Hume, D. A., Kamitani, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombae, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyohara, K., Wang, K. H., Weltz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohlsu, S. and Hayashizaki, Y.	
CONSTRM		RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium	
TITLE		Functional annotation of a full-length mouse cDNA collection	
JOURNAL		Nature 409 (6821), 685-690 (2001)	
PUBMED		11217851	
REFERENCE			
AUTHORS		5 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Oshino, N., Saito, R., Suzuki, H., Yamataka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,	

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GenCore version 5.1.9
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2815.117 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
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2	559	90.6	474	2	US-08-653-402B-9
3	498	80.7	484	3	US-10-226-795-31
4	486.5	78.8	360	2	US-08-672-176A-1
5	479	77.6	717	2	US-08-553-497A-17
6	475.5	77.1	405	3	US-08-579-378A-15
7	474	76.8	3343	10	5453363-2
8	471	76.3	747	5	US-09-661-992B-83

9	470.5	76.3	888	5	US-09-661-992B-99	Sequence 99, Appl
10	470.5	76.3	978	5	US-09-661-992B-91	Sequence 91, Appl
11	470.5	76.3	2199	5	US-09-661-992B-89	Sequence 89, Appl
12	469	76.0	357	2	US-08-331-398A-21	Sequence 21, Appl
13	469	76.0	357	2	US-08-331-397B-21	Sequence 21, Appl
14	469	76.0	357	2	US-08-759-804A-21	Sequence 21, Appl
15	469	76.0	357	3	US-09-227-693-21	Sequence 21, Appl
16	469	76.0	375	2	US-08-331-398A-59	Sequence 59, Appl
17	469	76.0	375	2	US-08-331-397B-59	Sequence 59, Appl
18	469	76.0	375	2	US-08-759-804A-58	Sequence 58, Appl
19	468	75.9	414	2	US-08-379-057-13	Sequence 13, Appl
20	467	75.7	351	3	US-09-339-922A-5	Sequence 5, Appl
21	467	75.7	351	3	US-08-791-391A-5	Sequence 5, Appl
22	467	75.7	351	3	US-09-016-061-5	Sequence 5, Appl
23	465	75.4	923	7	PCT-US94-07659-1	Sequence 1, Appl
24	464.5	75.3	783	3	US-08-487-283A-19	Sequence 19, Appl
25	464	75.2	711	4	US-10-073-301A-8	Sequence 8, Appl
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41	452.5	73.3	747	5	US-09-661-992B-87	Sequence 87, Appl
42	451.5	73.2	747	5	US-09-661-992B-85	Sequence 85, Appl
43	451	73.1	357	2	US-08-475-000-15	Sequence 15, Appl
44	451	73.1	357	2	US-08-483-199-15	Sequence 15, Appl
45	451	73.1	357	2	US-08-484-508-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-653-402B-5
; Sequence 5, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSEBL, Elisabeth
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; TITLE OF INVENTION: Immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995

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ATTORNEY/AGENT INFORMATION:
NAME: Lebowitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1781
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: monoclonal anti-idiotypic anti-EGFR antibody
INDIVIDUAL ISOLATE: 5A6 heavy chain
FEATURE:
NAME/KEY: CDS
LOCATION: 1..474
US-08-653-402B-5

Alignment Scores:
Pred. No.: 3,11e-65 Length: 474
Score: 559.00 Matches: 111
Percent Similarity: 92.8% Conservative: 5
Best Local Similarity: 98.8% Mismatches: 3
Query Match: 90.6% Indels: 6
DB: 2 Gaps: 2

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QY 21 SerCysAlaIaIaSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgLInThr 40
Db 118 TCCGTGTCAACCTCTGGATTCACTTTCAGTAATATTCATATCTCTGGGTTCGCAGACT 177
QY 41 ProGluLysArgLeuGluGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
Db 178 CCAGAGGAAGGCTGGAGTTGTGCGACGCAATTAATAGTAAGTGGTAGACCTACTAT 237
QY 61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
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Db 418 GTCACGCTCTCTCA 432

RESULT 2
US-08-653-402B-9
/ Sequence 9, Application US/08653402B
/ Patent No. 5969107
/ GENERAL INFORMATION:
/ APPLICANT: CARCELLER, Ana
/ APPLICANT: ROSSELL, Elisabeth
/ APPLICANT: GOMEZ, Alicia
/ APPLICANT: ADEN, Jaume
/ APPLICANT: PIULATS, Jaume
/

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1 TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
2 TITLE OF INVENTION: Immune response against epidermal growth factor receptor
3 NUMBER OF SEQUENCES: 13
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Millen, White, Zejano & Branigan, P.C.
6 STREET: 2200 Clarendon Boulevard, Suite 1400
7 CITY: Arlington
8 STATE: Virginia
9 COUNTRY: U.S.A.
10 ZIP: 22201
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12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/653,402B
18 FILING DATE: 24-MAY-1996
19 CLASSIFICATION: 435
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21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: EP 95107967.2
23 FILING DATE: 26-MAY-1995
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Lepovltz, Richard M.
26 REGISTRATION NUMBER: 37,067
27 REFERENCE/DOCKET NUMBER: MERCK 1781
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 703-243-6333
30 TELEFAX: 703-243-6410
31 INFORMATION FOR SEQ ID NO: 9:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 474 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: cDNA
38 HYPOTHETICAL: NO
39 ANTI-SENSE: NO
40 FRAGMENT TYPE: N-terminal
41 ORIGINAL SOURCE:
42 ORGANISM: monoclonal anti-idiotypic anti-BGFR antibody
43 INDIVIDUAL ISOLATE: 3B6 heavy chain
44 FEATURE:
45 NAME/KEY: CDS
46 LOCATION: 1..474
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50 Alignment Scores:
51 Pred. No.: 3,11e-65 Length: 474
52 Score: 559.00 Matches: 111
53 Percent Similarity: 92.8% Conservative: 5
54 Best Local Similarity: 88.8% Mismatches: 3
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VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 1:
US-08-672-176A-1

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Query Match: 78.8% Indels: 5
DB: 2 Gaps: 2

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RESULT 5
US-08-553-497A-17
Sequence 17, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANGELL, KEITH H.
APPLICANT: GUSSON, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELI, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PILATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: mouse
STRAIN: Balb/c
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: splenocytes
IMMEDIATE SOURCE:
CLONE: 4 B 2
FEATURE:
NAME/KEY: CDS
LOCATION: 1..717
US-08-553-497A-17

Alignment Scores:
Pred. No.: 2, 53e-54 Length: 717
Score: 479.00 Matches: 93
Percent Similarity: 88.2% Conservative: 12
Best Local Similarity: 78.2% Mismatches: 14
Query Match: 77.6% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-6 (1-119) x US-08-553-497A-17 (1-717)

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DB 21 SerCyAlaIaISerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnThr 40
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QY 41 ProGluYeaArgLeuGluIleuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
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181 CCAGACAGGTGTGAAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCTCTGTAC 240
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Db 241 CTGCAATATGACGCTGTGAAGTGTGAGACACAGCCATGATATACGTGCAAGACTTGA 300

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Db 301 ACCGGGAGACTATGCTTGTGACTACTGGGCGCAAGGACACGCTCACCGTCTCTCA 357

RESULT 6

US-08-579-378A-15
Sequence 15, Application US/08579378A

Patent No. 6210671

GENERAL INFORMATION:

APPLICANT: Co, Man Sung

TITLE OF INVENTION: Humanized Antibodies Reactive with

TITLE OF INVENTION: L-Selectin

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/579,378A

FILING DATE: 27-DEC-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/160,074

FILING DATE: 30-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/983,946

FILING DATE: 01-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95112895.8

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95114696.8

FILING DATE: 19-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Liebescheutz, Joe O.

REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 11823-002220

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 405 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..405

US-08-579-378A-15

Alignment Scores:

Pred. No.: 3.33e-54

Score: 475.50

Percent Similarity: 88.2%

Best Local Similarity: 79.8%

Query Match: 77.1%

DB: 3

US-10-635-908-6 (1-119) x US-08-579-378A-15 (1-405)

QY 1 AspValIleValLeuValGluSerGlyGlyIleValValIleValLeuValGlySerLeuValLeu 20

Db 58 GAAGTCAAGCTGTGAGTGTGAGGAGGCTTGAAGAGCTGGAGGGCTCTGAAACTC 117

QY 21 SerCysAlaIleSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40

Db 118 GCCTGTGCGCTCTGAGATTCACTTTCAGTACTTATGCCATGTCTTGGTTGCCAGACT 177

QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60

Db 178 CCAGAGAAAGGCTGGAGTGGGTCCGATCATTT---AGTACGTGTGTAGCACTACTAT 234

QY 61 LeuAspThrValIleGlyValArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTyr 80

Db 235 CCAGACAGTGTGAAGGCGGATTCACCATCTCCAGATTAATGCCAGAACTCTGTAC 294

QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100

Db 295 CTGCAATATGACGCTGTGAGTGTGAGGACGCGCATGTATTACTGTGCAAGACTAT 354

QY 101 SerGlyTyrPheSerMetAspTyrTrpGlyGlyGlyThrSerValThrValSerSer 119

Db 355 GACGGGTATTTT-----GACTACTGGGGCAAGCACCACCTCTCACAGTCTCTCA 405

RESULT 7

5453363-2

Patent No. 5453363

APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RAUF

TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR

ING AFTER GENETIC EXPRESSION IN PROKARYOTES

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206,044

FILING DATE: 02-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 942,370

FILING DATE: 09-SEP-1992

APPLICATION NUMBER: 498,500

FILING DATE: 23-MAR-1990

APPLICATION NUMBER: 76,207

FILING DATE: 23-OCT-1986

SEQ ID NO:2

LENGTH: 3343

5453363-2

Alignment Scores:

Pred. No.: 1e-52

Score: 474.00

Percent Similarity: 85.4%

Best Local Similarity: 76.4%

Query Match: 76.8%

DB: 10

US-10-635-908-6 (1-119) x 5453363-2 (1-3343)

QY 1 AspValIleValLeuValGluSerGlyGlyIleValValIleValLeuValGlySerLeuValLeu 20

Db 240 GAAGTCAAGCTGTGAGTGTGAGGAGGCTTGAAGAGCTGGAGGGCTCTGAAACTC 299

QY 21 SerCysAlaIleSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40

Db 300 TCCGTGTGACCCCTCTGATTCACCTTTCAGTACTTATGCCATGTCTTGGTTGCCAGACT 359

QY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60

Db 360 CCGGAAAAGGCTGGAGTGGGTCCGACCATTTAGTATGTGTAGTACCTACTAT 419

QY 61 LeuAspThrValIleGlyValArgPheThrIleSerArgAspAsnAlaIleAsnThrLeuTyr 80

Db 420 CCAGACAGTGTGAAGGCGGATTCACCATCTCCAGATTAATGCCAGAACTCTGTAC 479

QY 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100

Db 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100

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Db      480 CTCGAATGAGAGTGTGAGTGTGATGACAGCAGCATGTATTACTGTGCAAGATAG 539
Qy      101 SerGlyTyr-----PheSerMetAspTyrTyrGlyGlnGlyThrSerValThr 116
          :::::|||||
Db      540 GCGTACTATGAGTAACAGCGGAGCTGTATGAGTACTACTGGGGTCAAGAACTCTAGTACCC 599
Qy      117 ValSerSer 119
          |||||
Db      600 GTCTCTCTCA 608

RESULT 8
US-09-661-992B-83
/ Sequence 83, Application US/09661992B
/ Patent No. 7033590
/ GENERAL INFORMATION:
/ APPLICANT: Schefflinger, Friedrich
/ APPLICANT: Kerschbaumer, RandoIf
/ APPLICANT: Falkner, Falko-Guenther
/ APPLICANT: Dörner, Friedrich
/ APPLICANT: Baxter Aktiengesellschaft
/ TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
/ FILE REFERENCE: 20695C-005900US
/ CURRENT APPLICATION NUMBER: US/09/661,992B
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: AT A157600
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 83
/ LENGTH: 747
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: scFv from
US-09-661-992B-83

Alignment Scores:
Pred. No.:      3,11e-53      Length:      747
Score:          471.00      Matches:      95
Percent Similarity: 86.0%      Conservative: 9
Best Local Similarity: 78.5%      Mismatches: 15
Query Match:    76.3%      Indels:      2
DB:             5          Gaps:      2

US-10-635-908-6 (1-119) x US-09-661-992B-83 (1-747)
Qy      1 AspValIysLeuValGlnSerGlyGlyLeuValIysLeuGlySerLeuIysLeu 20
          :::::|||||
Db      1 GAAGTGCAGCTGTGAGTGTGAGGAGGCTGTAGTGAAGCTTGAGAGGTCCTGAAATC 60
Qy      21 SerCysAlaIaIaSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
          :::::|||||
Db      61 TCTGTGACAGCTCTGGATTCACTTTCAGTACCTATTCATGTCTTGCGTTCCGCAACT 120
Qy      41 ProGluIysArgLeuGlnLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
          :::::|||||
Db      121 CCGGAAGAAGAGCTGTGAGTGTGCGAACCATTAAGTGTGTGTTACACTTACTAT 180
Qy      61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
          :::::|||||
Db      181 CCGAGACAGTGTGAGGCGCATTCACATCTCCAGAGACATGCCAAGAACCCCTGTAC 240
Qy      81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
          :::::|||||
Db      241 CTCGAATGAGAGTGTGAGTGTGAGGACACAGCCTGATTAATCTGTAACAGAGATGG 300
Qy      101 Ser---GlyTyr---PheSerMetAspTyrTyrGlyGlnGlyThrSerValThrValSer 118
          :::::|||||
Db      301 GGAACAGCGGTACGTAGTACTTGTACTGTGGGCGCAAGCACCACTTCACAGTCTCC 360
Qy      119 Ser 119
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Db      361 TCA 363

RESULT 9
US-09-661-992B-99
/ Sequence 99, Application US/09661992B
/ Patent No. 7033590
/ GENERAL INFORMATION:
/ APPLICANT: Schefflinger, Friedrich
/ APPLICANT: Kerschbaumer, RandoIf
/ APPLICANT: Falkner, Falko-Guenther
/ APPLICANT: Dörner, Friedrich
/ APPLICANT: Baxter Aktiengesellschaft
/ TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
/ FILE REFERENCE: 20695C-005900US
/ CURRENT APPLICATION NUMBER: US/09/661,992B
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: AT A157600
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 99
/ LENGTH: 888
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:198AB2 scFv
/ OTHER INFORMATION: linked to c-myc-tag and His6 tag (ORF of
/ OTHER INFORMATION: expression vector pMyChis6-198AB2#102)
/ NAME/KEY: modified_base
/ LOCATION: (228)
/ OTHER INFORMATION: n = g, a, c or t
US-09-661-992B-99

Alignment Scores:
Pred. No.:      4,62e-53      Length:      888
Score:          470.50      Matches:      94
Percent Similarity: 84.4%      Conservative: 9
Best Local Similarity: 77.0%      Mismatches: 16
Query Match:    76.3%      Indels:      3
DB:             5          Gaps:      1

US-10-635-908-6 (1-119) x US-09-661-992B-99 (1-888)
Qy      1 AspValIysLeuValGlnSerGlyGlyLeuValIysLeuGlySerLeuIysLeu 20
          :::::|||||
Db      67 GAAGTGAAGCTGTGAGTGTGAGGAGGCTTAGTGAAGCTTGAGAGGTCCTGAAATC 126
Qy      21 SerCysAlaIaIaSerGlyPheThrPheSerAsnTyrTyrMetSerTyrValArgGlnThr 40
          :::::|||||
Db      127 TCTGTGACAGCTCTGGATTCACTTTCAGTACCTATTCATGTCTTGCGTTCCGCAACT 186
Qy      41 ProGluIysArgLeuGlnLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyr 60
          :::::|||||
Db      187 CCGGAAGAAGAGCTGTGAGTGTGCGAACCATTAAGTGTGTGTTACACTTACTAT 246
Qy      61 LeuAspThrValIysGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
          :::::|||||
Db      247 CCGAGACAGTGTGAGGCGCATTCACATCTCCAGAGACATGCCAAGAACCCCTGTAC 306
Qy      81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg 100
          :::::|||||
Db      307 CTCGAATGAGAGTGTGAGTGTGAGGACACAGCCTGATTAATCTGTAACAGAGAGGG 366
Qy      101 SerGlyTyr-----PheSerMetAspTyrTyrGlyGlnGlyThrSerValThrVal 117
          :::::|||||
Db      367 GGTGTTCACCTGACCTGATCTGATCTGTGGGCGGAGGAGACCTTCAGTACAGCTC 426
Qy      118 SerSer 119
          |||||
Db      427 TCCTCA 432
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```
RESULT 10
US-09-661-992B-91
; Sequence 91, Application US/09661992B
; Patent No. 7033590
; GENERAL INFORMATION:
; APPLICANT: Schering, Friedrich
; APPLICANT: Kerschbaumer, Randoif
; APPLICANT: Falko-Guenther
; APPLICANT: Dörner, Friedrich
; APPLICANT: Baxter Aktiengesellschaft
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/09/661,992B
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: AT A157600
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
; NAME/KEY: modified_base
; LOCATION: (1)..(978)
; OTHER INFORMATION: n = g, a, c or t
US-09-661-992B-91

Alignment Scores:
Pred. No.: 5,29e-53 Length: 978
Score: 470.50 Matches: 94
Percent Similarity: 84.4% Conservative: 9
Best Local Similarity: 77.0% Mismatches: 16
Query Match: 76.3% Indels: 3
DB: Gaps: 1

US-10-635-908-6 (1-119) x US-09-661-992B-91 (1-978)
QY 1 AspyVallylsleuValGlsuSerGlyGlyleuVallylsleuGlySerleuYsleu 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 67 GAGGTGAAGCTGGTGGAGCTCTGGGGAGGCTTAGTGAAGCTGAGGGCTCCCTGAACCTC 126
QY 21 SerCysAlaIaserglyPheThrPheSerAsnTyrrMetSerTrrpValargGlnThr 40
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 127 TCCTGTGACGCTCTGGATTCACTTTCAGTAGCTATACCATGCTCTGGGTTCCGCAGACT 186
QY 41 ProGluYsaArgleuGluValAlaAlaIleAsnSerAspGlyGlyIleThrTyrrTyrr 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 187 CCGGAGAAAGAGGCTGGAGTGGGTCCCAACCATTAAGTAGGAGTTCACCACTACTAT 246
QY 61 LeuAspThrVallylsGlyAArgPheThrIleSerArgAspAsnAlaYsAsnThrleuTyrr 80
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 247 CCAAGACAGTGAAGGGCCGATTCACCATCTCCAGAGACATGCCAAGAACCTCTGAC 306
QY 81 LeuGlnMetSerSerleuYsSerGluAspThrAlaIleuPheTyrrCysAlaArgHisArg 100
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 307 CTGCAAAATGACAGCTGAGCTCTGAGACACAGCCAGTATTAAGTACAAAGAGAGGG 366
QY 101 SerGlyTyrr-----PheSerMetAspTyrrTrrpGlyGlnGlyThrSerValThrVal 117
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 367 GGTGGTTTCACCGTCACACTGTAATCTGATGTCTGGGGCGCAGAGAACTCAGTCACCGTC 426
QY 118 SerSer 119
   |||||
DB 427 TCCTCA 432

RESULT 11
US-09-661-992B-89
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; Sequence 89, Application US/09661992B
; Patent No. 7033590
; GENERAL INFORMATION:
; APPLICANT: Schering, Friedrich
; APPLICANT: Kerschbaumer, Randoif
; APPLICANT: Falko-Guenther
; APPLICANT: Dörner, Friedrich
; APPLICANT: Baxter Aktiengesellschaft
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/09/661,992B
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: AT A157600
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 2199
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:198A2
; OTHER INFORMATION: scFv-alkaline phosphatase fusion protein (ORF of
; OTHER INFORMATION: expression vector pDAP2-198AB2#100)
; NAME/KEY: modified_base
; LOCATION: (228)
; OTHER INFORMATION: n = g, a, c or t
US-09-661-992B-89

Alignment Scores:
Pred. No.: 1,64e-52 Length: 2199
Score: 470.50 Matches: 94
Percent Similarity: 84.4% Conservative: 9
Best Local Similarity: 77.0% Mismatches: 16
Query Match: 76.3% Indels: 3
DB: Gaps: 1

US-10-635-908-6 (1-119) x US-09-661-992B-89 (1-2199)
QY 1 AspyVallylsleuValGlsuSerGlyGlyleuVallylsleuGlySerleuYsleu 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 67 GAGGTGAAGCTGGTGGAGCTCTGGGGAGGCTTAGTGAAGCTGAGGGCTCCCTGAACCTC 126
QY 21 SerCysAlaIaserglyPheThrPheSerAsnTyrrMetSerTrrpValargGlnThr 40
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 127 TCCTGTGACGCTCTGGATTCACTTTCAGTAGCTATACCATGCTCTGGGTTCCGCAGACT 186
QY 41 ProGluYsaArgleuGluValAlaAlaIleAsnSerAspGlyGlyIleThrTyrrTyrr 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 187 CCGGAGAAAGAGGCTGGAGTGGGTCCCAACCATTAAGTAGGAGTTCACCACTACTAT 246
QY 61 LeuAspThrVallylsGlyAArgPheThrIleSerArgAspAsnAlaYsAsnThrleuTyrr 80
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 247 CCAAGACAGTGAAGGGCCGATTCACCATCTCCAGAGACATGCCAAGAACCTCTGAC 306
QY 81 LeuGlnMetSerSerleuYsSerGluAspThrAlaIleuPheTyrrCysAlaArgHisArg 100
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 307 CTGCAAAATGACAGCTGAGCTCTGAGACACAGCCAGTATTAAGTACAAAGAGAGGG 366
QY 101 SerGlyTyrr-----PheSerMetAspTyrrTrrpGlyGlnGlyThrSerValThrVal 117
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 367 GGTGGTTTCACCGTCACACTGTAATCTGATGTCTGGGGCGCAGAGAACTCAGTCACCGTC 426
QY 118 SerSer 119
   |||||
DB 427 TCCTCA 432

RESULT 12
US-08-331-398A-21
; Sequence 21, Application US/08331398A
; Patent No. 5608039
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 3, 2006, 06:54:05 ; Search time 817.991 Seconds
(without alignments)
2681.378 Million cell updates/sec

Title: US-10-635-908-6
Perfect score: 617
Sequence: 1 DVKLVESGGGLVKGSLKLT.....RSGYFSMDYWGQGTSTVTS 119

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS-human40.cdi -LIST=45 -OCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abses02h
-USER=US10635908.@CGN_1_1_2326@runat.02062006.104222.10380 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.Main:*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No. Query Match Length DB ID Description
1 617 100.0 357 8 US-10-470-940-1 Sequence 1, Appli

2 617 100.0 357 9 US-10-635-908-5 Sequence 5, Appli
3 617 100.0 1056 8 US-10-333-235A-8 Sequence 8, Appli
4 617 100.0 1411 8 US-10-333-235A-10 Sequence 10, Appli
5 617 100.0 1702 8 US-10-333-235A-11 Sequence 11, Appli
6 617 100.0 2431 9 US-10-635-908-9 Sequence 9, Appli
7 605 98.1 444 11 US-10-504-389A-50 Sequence 50, Appli
8 498 80.7 484 8 US-10-226-795-31 Sequence 31, Appli
9 495 80.2 466 3 US-09-881-823-11 Sequence 11, Appli
10 495 80.2 533 3 US-09-910-358D-5 Sequence 5, Appli
11 495 80.2 533 8 US-10-077-624-5 Sequence 5, Appli
12 495 80.2 533 8 US-10-077-624-5 Sequence 5, Appli
13 495 80.2 563 3 US-09-910-358D-1 Sequence 1, Appli
14 495 80.2 563 7 US-10-077-624-1 Sequence 1, Appli
15 495 80.2 563 8 US-10-706-391-1 Sequence 1, Appli
16 482 78.1 374 7 US-10-169-351-66 Sequence 66, Appli
17 482 78.1 756 7 US-10-169-351-68 Sequence 68, Appli
18 481 78.0 1386 7 US-10-281-479A-21 Sequence 21, Appli
19 481 78.0 1386 7 US-10-286-132A-21 Sequence 21, Appli
20 481 78.0 1398 7 US-10-275-180A-21 Sequence 21, Appli
21 480.5 77.9 360 8 US-10-383-447-5 Sequence 5, Appli
22 478 77.5 363 7 US-10-300-215-88 Sequence 88, Appli
23 478 77.5 369 10 US-10-490-535-1 Sequence 1, Appli
24 478 77.5 420 3 US-09-286-240-3 Sequence 3, Appli
25 472 76.5 414 7 US-10-010-942B-3 Sequence 3, Appli
26 472 76.5 414 8 US-10-388-389-3 Sequence 3, Appli
27 472 76.5 414 8 US-10-703-713-3 Sequence 3, Appli
28 472 76.5 414 8 US-10-704-070-3 Sequence 3, Appli
29 472 76.5 414 9 US-10-232-030-3 Sequence 3, Appli
30 472 76.5 414 10 US-10-789-273-3 Sequence 3, Appli
31 471 76.3 747 13 US-11-093-103-83 Sequence 83, Appli
32 470.5 76.3 888 13 US-11-093-103-99 Sequence 99, Appli
33 470.5 76.3 978 13 US-11-093-103-91 Sequence 91, Appli
34 470.5 76.3 2199 13 US-11-093-103-89 Sequence 89, Appli
35 468 75.9 766 7 US-10-258-728-1 Sequence 1, Appli
36 467.5 75.8 746 8 US-10-354-246-3 Sequence 3, Appli
37 467 75.7 351 2 US-08-790-540A-5 Sequence 5, Appli
38 467 75.7 351 2 US-08-791-391A-5 Sequence 5, Appli
39 467 75.7 351 3 US-09-900-590-5 Sequence 5, Appli
40 467 75.7 351 7 US-10-305-231-5 Sequence 5, Appli
41 467 75.7 351 7 US-10-452-440-5 Sequence 5, Appli
42 467 75.7 351 7 US-10-463-847-5 Sequence 5, Appli
43 467 75.7 351 10 US-10-959-871-5 Sequence 5, Appli
44 465 75.4 345 8 US-10-436-782-45 Sequence 45, Appli
45 465 75.4 345 8 US-10-436-783-13 Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-10-470-940-1
; Sequence 1, Application US/10470940
; Publication No. US20040077081A1
GENERAL INFORMATION:
; APPLICANT: Oosterwijk, Egbert
; APPLICANT: Wernaar, Sven
; APPLICANT: Ullrich, Stefan
; TITLE OF INVENTION: Hybridoma Cell line G250 and its use for producing monoclonal
; TITLE OF INVENTION: antibodies
; FILE REFERENCE: 2923-0548
; CURRENT APPLICATION NUMBER: US/10/470,940
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01282
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/266853
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/327008
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Artificial Sequence

US-10-635-908-6 (1-119) x US-10-333-235A-8 (1-1056)

```
QY 1 AspvAllyleuValGluSerGlyGlyLeuVallyleuGluGlySerLeuysleu 20
DB 376 GACGTAAAGCTCGTGAAGTCTGGGGAGGCTTAGTAAGCTTGAGAGGCTCCGTAACCTC 435
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyTrpMetSerTrpValArgGlnThr 40
DB 436 TCTGTGACGACCTCTGGATTCACTTTCAGTAACATACTGCTGGGTGGCCAGACT 495
QY 41 ProGluYArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyTrp 60
DB 496 CCAGAGAAAGAGGCTGGAGTTGGTCGACCATTAATAGATGGTGGTATCACTACTAT 555
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyR 80
DB 556 CTAGACACCTGTGAAGGCCGATTCACCATTTCAAGAGACAAATGCCAAGAACACCCCTGTAC 615
QY 81 LeuGlnMetSerSerLeuIysSerGlyAspThrAlaLeuPheTyrcysAlaArgHisArg 100
DB 616 CTGCATAATGACAGCTGTAAGTCTGAGGACACAGCCTTGTTTACTGTGCAAGACACCCG 675
QY 101 SerGlyTyTrpPheSerMetAspTyTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 676 TCGGGCTACTTTTCTATGACACTCTGGGGCTCAAGAAACCTCAGTCAACGCTCTCTCA 732
```

RESULT 4

```
US-10-333-235A-10
; Sequence 10, Application US/10333235A
; Publication No. US20040132007A1
; GENERAL INFORMATION:
; APPLICANT: GOF-A-GENE AB
; APPLICANT: Leif, Lindholm
; APPLICANT: Karin, Nord
; APPLICANT: Pierre, Boulanger
; APPLICANT: Rebecca, Gardner
; TITLE OF INVENTION: Modified Virus
; FILE REFERENCE: 9.7.72728/001
; CURRENT APPLICATION NUMBER: US/10/333,235A
; CURRENT FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fiber construct A1 G250
US-10-333-235A-10
```

Alignment Scores:

Pred. No.:	2.55e-75	Length:	1411
Score:	617.00	Matches:	119
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0

US-10-635-908-6 (1-119) x US-10-333-235A-10 (1-1411)

```
QY 1 AspvAllyleuValGluSerGlyGlyLeuVallyleuGluGlySerLeuysleu 20
DB 722 GACGTAAAGCTCGTGAAGTCTGGGGAGGCTTAGTAAGCTTGAGAGGCTCCGTAACCTC 781
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyTrpMetSerTrpValArgGlnThr 40
DB 782 TCTGTGACGACCTCTGGATTCACTTTCAGTAACATACTGCTGGGTGGCCAGACT 841
QY 41 ProGluYArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyTrp 60
DB 842 CCAGAGAAAGAGGCTGGAGTTGGTCGACCATTAATAGATGGTGGTATCACTACTAT 901
```

```
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyR 80
DB 902 CTAGACACCTGTGAAGGCCGATTCACCATTTCAAGAGACAAATGCCAAGAACACCCCTGTAC 961
QY 81 LeuGlnMetSerSerLeuIysSerGlyAspThrAlaLeuPheTyrcysAlaArgHisArg 100
DB 962 CTGCATAATGACAGCTGTAAGTCTGAGGACACAGCCTTGTTTACTGTGCAAGACACCCG 1021
QY 101 SerGlyTyTrpPheSerMetAspTyTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 1022 TCGGGCTACTTTTCTATGACACTCTGGGGCTCAAGAAACCTCAGTCAACGCTCTCTCA 1078
```

RESULT 5

```
US-10-333-235A-11
; Sequence 11, Application US/10333235A
; Publication No. US20040132007A1
; GENERAL INFORMATION:
; APPLICANT: GOF-A-GENE AB
; APPLICANT: Leif, Lindholm
; APPLICANT: Karin, Nord
; APPLICANT: Pierre, Boulanger
; APPLICANT: Rebecca, Gardner
; TITLE OF INVENTION: Modified Virus
; FILE REFERENCE: 9.7.72728/001
; CURRENT APPLICATION NUMBER: US/10/333,235A
; CURRENT FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1702
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fiber construct A7 G250
US-10-333-235A-11
```

Alignment Scores:

Pred. No.:	3.34e-75	Length:	1702
Score:	617.00	Matches:	119
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0

US-10-635-908-6 (1-119) x US-10-333-235A-11 (1-1702)

```
QY 1 AspvAllyleuValGluSerGlyGlyLeuVallyleuGluGlySerLeuysleu 20
DB 1013 GACGTAAAGCTCGTGAAGTCTGGGGAGGCTTAGTAAGCTTGAGAGGCTCCGTAACCTC 1072
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyTrpMetSerTrpValArgGlnThr 40
DB 1073 TCTGTGACGACCTCTGGATTCACTTTCAGTAACATACTGCTGGGTGGCCAGACT 1132
QY 41 ProGluYArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyTrp 60
DB 1133 CCAGAGAAAGAGGCTGGAGTTGGTCGACCATTAATAGATGGTGGTATCACTACTAT 1192
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyR 80
DB 1193 CTAGACACCTGTGAAGGCCGATTCACCATTTCAAGAGACAAATGCCAAGAACACCCCTGTAC 1252
QY 81 LeuGlnMetSerSerLeuIysSerGlyAspThrAlaLeuPheTyrcysAlaArgHisArg 100
DB 1253 CTGCATAATGACAGCTGTAAGTCTGAGGACACAGCCTTGTTTACTGTGCAAGACACCCG 1312
QY 101 SerGlyTyTrpPheSerMetAspTyTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 1313 TCGGGCTACTTTTCTATGACACTCTGGGGCTCAAGAAACCTCAGTCAACGCTCTCTCA 1369
```

RESULT 6

US-10-635-908-9
; Sequence 9, Application US/10635908

US-10-635-908-6 (1-119) x US-10-226-795-31 (1-484)

```
QY 1 AspvallyleuValgluSerGlyglYleuVallyleuGlYglYserleuYleu 20
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 GAAGTCAGAGCTGGAGTCGTGGGGAGGCTGTAGTAAGCTGGAGGGTCCCGAAATC 125
QY 21 SerCysAlaIaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnTr 40
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 TCTGTGACAGCTCTGGATTGCTTTCAGCTAGCTAGACATGCTTGGGTCCCGACT 185
QY 41 ProGluYleArgleuGluLeuValAlaAlaIleAsnSerAspGlyglYleuTrpTYr 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 CCGAGAAAGAGGCTGGAGTGGGTCCGATACATTAGTCGTGTGGTTACCTACTAT 245
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrleuTYr 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 CCAGACACTGTGAAGGCCGATTCACCATCTCCAGAGACAAATCCAAAGAACCTGTATC 305
QY 81 LeuGluMetSerSerleuYleuYleuSerGluAspThrAlaIleuPheTYrCysAlaArgHis 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 CTGCAAAATGAGCTGAGCTGAGGACACAGCCATGATTAATCTGTTCAAGACATATA 365
QY 100 -----ArgSerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThr 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 366 TATTACGGAGCTGTCTATTCTATGCTATGACTGACTGGGTCAAGGAACCTCAGTCACC 425
QY 117 ValSerSer 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 426 GTCTCTTCA 434
```

RESULT 9

```
US-09-881-823-11
; Sequence 11, Application US/09881823
; Patent No. US2002006806A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(442)
US-09-881-823-11
```

Alignment Scores:

```
Pred. No.: 6,8e-59 Length: 466
Score: 495.00 Matches: 98
Percent Similarity: 88.6% Conservative: 11
Best Local Similarity: 79.7% Mismatches: 10
Query Match: 80.2% Indels: 4
DB: 3 Gaps: 1
```

US-10-635-908-6 (1-119) x US-09-881-823-11 (1-466)

```
QY 1 AspvallyleuValgluSerGlyglYleuVallyleuGlYglYserleuYleu 20
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 GACGTGAAGCTGTGGAGCTGTGGGGAGGCTTAGTGAACCTTGAGGGTCTCTGAAACTC 127
```

```
QY 21 SerCysAlaIaSerGlyPheThrPheSerAsnTYrTYrMetSerTrpValArgGlnTr 40
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 TCTGTGACAGCTCTGGATTGCTTTCAGCTAGCTAGACATGCTTGGGTCCCGACT 187
QY 41 ProGluYleArgleuGluLeuValAlaAlaIleAsnSerAspGlyglYleuTrpTYr 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 CCGAGAAAGAGGCTGGAGTGGGTCCGATTCATTAGTAGTGCTAGCTTACACTACTAT 247
QY 61 LeuAspThrVallyleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrleuTYr 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 CCAGACAGTGAAGGCCGATTCACCATCTCCAGAGACAAATGCCAAAGAACCTGTATC 307
QY 81 LeuGluMetSerSerleuYleuYleuSerGluAspThrAlaIleuPheTYrCysAlaArg 98
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 CTGCAAAATGACAGCTGAGCTGAGGACACAGCCATGATTAATCTGTTCAAGAGATGAC 367
QY 99 -----HisArgSerGlyTYrPheSerMetAspTYrTrpGlyGlnGlyThrSerValThr 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 GGCTCTACGGCTCTATTACTATGCTATGACTACTGGGGTCAAGGAACCTCAGTCACC 427
QY 117 ValSerSer 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 428 GTCTCTTCA 436
```

RESULT 10

```
US-09-910-358D-5
; Sequence 5, Application US/0910358D
; Publication No. US2004005281A1
; GENERAL INFORMATION:
; APPLICANT: Shi, WenYuan
; APPLICANT: Anderson, Maxwell
; APPLICANT: Morrison, Sherie
; APPLICANT: Trinh, Kham
; APPLICANT: Wims, Letitia
; APPLICANT: Chen, Li
; TITLE OF INVENTION: Fusion Proteins for Targeted Delivery of Antimicrobial Peptides
; FILE REFERENCE: 22851-033
; CURRENT APPLICATION NUMBER: US/09/910,358D
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized using sequential PCR techniques
; NAME/KEY: CDS
; LOCATION: (69)..(110)
; OTHER INFORMATION: Dvvar 1
; NAME/KEY: CDS
; LOCATION: (111)..(158)
; OTHER INFORMATION: Linker Peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (159)..(533)
; OTHER INFORMATION: VH of SWLA3
US-09-910-358D-5
```

Alignment Scores:

```
Pred. No.: 8,23e-59 Length: 533
Score: 495.00 Matches: 98
Percent Similarity: 88.6% Conservative: 11
Best Local Similarity: 79.7% Mismatches: 10
Query Match: 80.2% Indels: 4
DB: 3 Gaps: 1
```

US-10-635-908-6 (1-119) x US-09-910-358D-5 (1-533)

Qy	1	AspValIyLeuValIGIuSerGIyGIyLeuValIyLeuGIyGIySerLeuIySleu	20
Db	159	GAGGTAAAGCTTGTGAGTCTGGGGAGGCTTAGTAACCTGGAGGGTCCGTGAAC	218
Qy	21	SerCyAlaIaISerGIyPheThrPheSerAsnTYrTYrMetSerTriValArgIthr	40
Db	219	TCCTGTGAGCCTCTGGATTCACTTTCAGTAGCTAACATGTCTTGCGGCTCCGACACT	278
Qy	41	ProGIuIyArGIeGIuIyValIaIaIaIeASerSAspGIyGIyIleThTYrTYr	60
Db	279	CCGGAGAAGAGCTGGAGTGGGTGGCATCATTAGTGGTGGTACTTAACACTCTAT	338
Qy	61	LeuAspThrValIyLeGIyArGPheThrIISerArGAspAsnAlaIySAnthLeuTYr	80
Db	339	CCAGACAGGTGAAGGGCCGATTCACTCCAGAGACAATGCCAAGAACAACCTGTAC	398
Qy	81	LeuGIuMetSerSerIeulysSerGIuAspThrAlaIeulPheTYrCyAlaArg-----	98
Db	399	CTGCAAAATGACCAAGTCTGAAGCTGTGGAGCACAGCATATTATTCGTTCCAAAGATGAC	458
Qy	99	-----HIeArGIerGIyTYrPheSerMetAspTYrTriPGIyGIyIleThTYrSerValThr	116
Db	459	GGCTCTCAGGCTCTCATTTACTATGCTATGACTACTGGGGTCAAGAACTCAGTCACC	518
Qy	117	ValSerSer 119	
Db	519	GTCTCTTCA 527	
RESULT 11			
US-10-077-624-5			
/ Sequence 5, Application US/10077624			
/ Publication No. US20030143234A1			
/ GENERAL INFORMATION:			
/ APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA			
/ APPLICANT: WASHINGTON DENTAL SERVICE			
/ APPLICANT: Shi, Wenyuan			
/ APPLICANT: Anderson, Maxwell			
/ APPLICANT: Morrison, Sherie			
/ APPLICANT: Trinh, Kham			
/ APPLICANT: Wims, Letitia			
/ APPLICANT: Chen, Li			
/ TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL			
/ FIDE REFERENCE: 2101363-991200			
/ CURRENT APPLICATION NUMBER: US/10/077,624			
/ CURRENT FILING DATE: 2002-02-14			
/ PRIOR APPLICATION NUMBER: US 09/910,358			
/ PRIOR FILING DATE: 2001-07-19			
/ PRIOR APPLICATION NUMBER: US 09/378,577			
/ PRIOR FILING DATE: 1999-08-20			
/ NUMBER OF SEQ ID NOS: 31			
/ SOFTWARE: PatentIn version 3.1			
/ SEQ ID NO 5			
/ LENGTH: 533			
/ TYPE: DNA			
/ ORGANISM: Artificial sequence			
/ FEATURE:			
/ OTHER INFORMATION: Synthesized using sequential PCR techniques			
US-10-077-624-5			
Alignment Scores:			
Pred. No.: 8,23e-59 Length: 533			
Score: 495.00 Matches: 98			
Percent Similarity: 88.6% Conservative: 11			
Best Local Similarity: 79.7% Mismatches: 10			
Query Match: 80.2% Indels: 4			
DB: 7 Gaps: 1			
US-10-635-908-6 (1-119) x US-10-077-624-5 (1-533)			
Qy	1	AspValIyLeuValIGIuSerGIyGIyLeuValIyLeuGIyGIySerLeuIySleu	20
Db	159	GAGGTAAAGCTTGTGAGTCTGGGGAGGCTTAGTAACCTGGAGGGTCCGTGAAC	218

```

Oy      21 SerCyaaIaaIaaSerGlyPheThrPheSerAenYrYrMetSerTrpValargInthr 40
Db      219 TCCTGTGACGCTCTGAGATTCACCTTCAGTACGCTATACCATCTCTGGTTCGCCAGACT 278
Oy      41 ProGluYsArgLeuGluLeuValaIaaIaaIleasnSerAaspGlyIleThrYrYr 60
Db      279 CCGAAGAAGAGAGGCTGAGAGTGGGTCCCAATCCATTAAGTGGGTGATTAACACTAT 338
Oy      61 LeuapThrValLysValArgPheThrIleSerAgaAaspAaaIaIysaenThrLeuYr 80
Db      339 CCAAGACATGTGAAGAGGCCGATTAACCAATCTCCAGACAAATGCCAAGAACCCCTGAC 398
Oy      81 LeuGlnMetSerSerLeuLysSerGluApsThrIaIeupheYrCyaaIaaArg----- 98
Db      399 CTGCAAAATGACACAGCTGAGTCAAGCTGAGACACAGCCATGATTAATGCTTCAAGAGATGAC 458
Oy      99 -----HlaArgSerGlyYrPheSerMetApyrTrpGlyGlnGlyYrPheSerValThr 116
Db      459 GGCCTCTACGGCTCCTATTACTATGACTATGACTGCGGATCAAGAAACCTGACGACC 518
Oy      117 ValSerSer 119
Db      519 GTCTCTTCA 527

RESULT 12
US-10-706-391-3
; Sequence 3, Application US/10706391
; Publication No. US20040137482A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: WASHINGTON DENTAL SERVICE
; APPLICANT: Eckert, Randal
; APPLICANT: Qi, Fengxian
; APPLICANT: Shi, Wenyuan
; APPLICANT: Anderson, Maxwell H.
; TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
; FILE REFERENCE: 2101363-991600
; CURRENT APPLICATION NUMBER: US/10/706,391
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 10/077,624
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 09/910,358
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized using sequential PCR techniques
US-10-706-391-3

Alignment Scores:
Pred. No.:      8,23e-59      Length:      533
Score:          495.00      Matches:      98
Percent Similarity: 88.6%      Conservative: 11
Best Local Similarity: 79.7%      Mismatches:  10
Query Match:     80.2%      Indels:      4
DB:              8          Gaps:          1

US-10-635-908-6 (1-119) x US-10-706-391-3 (1-533)
Oy      1 AspValIysLeuValGluSerGlyGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20
Db      159 GACGGGAAGCTTGTGGAAGTCTGGGGAGGCTTAAGTAACCCCTGAGGGTCCCTGAACATC 218
Oy      21 SerCyaaIaaIaaSerGlyPheThrPheSerAenYrYrMetSerTrpValargInthr 40
Db      219 TCCTGTGACGCTCTGAGATTCACCTTCAGTACGCTATACCATCTCTGGTTCGCCAGACT 278

```


QY 41 ProGUlyArLeuValAlaAlaIleAsnSerAspGlyIleThrTyr 60
DB 279 CCGAGAAAGGCTGAGAGTGGCTGCATCTAGTAGTGTGTACTTACACTTACTAT 338
QY 61 LeuAspThrValIleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
DB 339 CCAGACAGGTGAAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACCCTGTAC 398
QY 81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTyrCysAlaArg----- 98
DB 399 CTGCAAAATGACCAAGTCTGAGAGTCTGAGACACAGCCATGATTACTGTCTCAAGAGATGAC 458
QY 99 -----HisArgSerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThr 116
DB 459 GGCCTCCTACGGCTCTTACTATGACTATGAGTCTACTGGGTCAAGAACTCAGTAC 518
QY 117 ValSerSer 119
DB 519 GTCTCTTCA 527
RESULT 13
US-09-910-358D-1
Sequence 1, Application US/09910358D
Publication No. US20040052814A1
GENERAL INFORMATION:
APPLICANT: Shi, Wenyan
APPLICANT: Anderson, Maxwell
APPLICANT: Morrison, Sherie
APPLICANT: Trinh, Khau
APPLICANT: Wims, Letitia
APPLICANT: Chen, Li
TITLE OF INVENTION: Fusion Proteins for Targeted Delivery of Antimicrobial Peptides
FILE REFERENCE: 22851-033
CURRENT APPLICATION NUMBER: US/09/910.358D
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 563
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: Synthesized using sequential PCR techniques
FEATURE:
NAME/KEY: CDS
LOCATION: (69)..(140)
OTHER INFORMATION: Histatin 5
FEATURE:
NAME/KEY: CDS
LOCATION: (141)..(188)
OTHER INFORMATION: Linker Peptide
FEATURE:
NAME/KEY: CDS
LOCATION: (189)..(563)
OTHER INFORMATION: VH of SWLA3
US-09-910-358D-1
Alignment Scores:
Pred. No.: 8.9e-59 Length: 563
Score: 495.00 Matches: 98
Percent Similarity: 88.6% Conservative: 11
Best Local Similarity: 79.7% Mismatches: 10
Query Match: 80.2% Indels: 4
DB: 3 Gaps: 1
US-10-635-908-6 (1-119) x US-09-910-358D-1 (1-563)
QY 1 AspValIysLeuValGlnSerGlyGlyIleValIysLeuGlyIleSerIleuValLeu 20
DB 189 GACGTGAAGCTTGTGAGCTGTGGGGAGGCTTAAAGAACTTGAGAGGCTCCCTGAACCTC 248

QY 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40
DB 249 TCCGTGACGCTTGAGATTCATCTTCACTACTACTATACCATATGTTGGGTGCCAGACT 308
QY 41 ProGUlyArLeuValAlaAlaIleAsnSerAspGlyIleThrTyrTyr 60
DB 309 CCGAGAAAGGCTGAGAGTGGCTGCATCTAGTAGTGTGTACTTACACTTACTAT 368
QY 61 LeuAspThrValIleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
DB 369 CCAGACAGGTGAAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACCCTGTAC 428
QY 81 LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTyrCysAlaArg----- 98
DB 429 CTGCAAAATGACCAAGTCTGAGAGTCTGAGACACAGCCATGATTACTGTCTCAAGAGATGAC 488
QY 99 -----HisArgSerGlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThr 116
DB 489 GGCCTCCTACGGCTCTTACTATGACTATGAGTCTACTGGGTCAAGAACTCAGTAC 548
QY 117 ValSerSer 119
DB 549 GTCTCTTCA 557
RESULT 14
US-10-077-624-1
Sequence 1, Application US/10077624
Publication No. US20030143234A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: WASHINGTON DENTAL SERVICE
APPLICANT: Shi, Wenyan
APPLICANT: Anderson, Maxwell
APPLICANT: Morrison, Sherie
APPLICANT: Trinh, Khau
APPLICANT: Wims, Letitia
APPLICANT: Chen, Li
APPLICANT: Qi, Fengxia
TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
FILE REFERENCE: 2101363-991200
CURRENT APPLICATION NUMBER: US/10/077,624
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 563
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE: Synthesized using sequential PCR techniques
OTHER INFORMATION:
US-10-077-624-1
Alignment Scores:
Pred. No.: 8.9e-59 Length: 563
Score: 495.00 Matches: 98
Percent Similarity: 88.6% Conservative: 11
Best Local Similarity: 79.7% Mismatches: 10
Query Match: 80.2% Indels: 4
DB: 7 Gaps: 1
US-10-635-908-6 (1-119) x US-10-077-624-1 (1-563)
QY 1 AspValIysLeuValGlnSerGlyGlyIleValIysLeuGlyIleSerIleuValLeu 20
DB 189 GACGTGAAGCTTGTGAGCTGTGGGGAGGCTTAAAGAACTTGAGAGGCTCCCTGAACCTC 248
QY 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40

Db 249 TCCTGTGACGCTCTGGATTCACTTTCAGTAGCTATACCATGTCTGGTTCGCCGACT 308
Qy 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyIleThrTyr 60
Db 309 CCGGAGAAAGGCTGTGAGTGGTGGCATCATTAAGTAGTGGTACTTACACTACTAT 368
Qy 61 LeuAspThrValIleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
Db 369 CCAGACAGGTGTGAAGGGCCGATTCACCATCTCCAGAGACAAATGCCAAGAACCTCTGTAC 428
Qy 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArg----- 98
Db 429 CTGCAAAATGACCATGTGAAGTCTGAGGACACAGCATATTAAGTCTTCAAGAGATGAC 488
Qy 99 -----HisArgSerGlyTyrPheSerMetAspTyrTTPGlyGlnGlyThrSerValThr 116
Db 489 GGCTCCTACGGCTCTATTACTATGACTATGACTACTGGGGTCAAGAAACCTCAGTCACC 548
Qy 117 ValSerSer 119
Db 549 GTCTCTTCA 557

RESULT 15

US-10-706-391-1
; Sequence 1, Application US/10706391
; Publication No. US20040137482A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: WASHINGTON DENTAL SERVICE
; APPLICANT: Eckert, Randall
; APPLICANT: Qi, Fengxia
; APPLICANT: Shi, Wenjuan
; APPLICANT: Anderson, Maxwell H.
; TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
; FILE REFERENCE: 2101363-991600
; CURRENT FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 10/077,624
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 09/910,358
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized using sequential PCR techniques
US-10-706-391-1

Alignment Scores:

Pred. No.: 8.9e-59 Length: 563
Score: 495.00 Matches: 98
Percent Similarity: 88.6% Conservative: 11
Best Local Similarity: 79.7% Mismatches: 10
Query Match: 80.2% Indels: 4
DB: 8 Gaps: 1

US-10-635-908-6 (1-119) x US-10-706-391-1 (1-563)

Qy 1 AspValLysLeuValGluSerGlyGlyLeuValLysLeuGlyGlySerLeuLysLeu 20
Db 189 GACGTAAAGCTTGTGAGTCTGGGGAGGCTTAGTGAACCTTGAGGGTCCCTGAAATC 248
Qy 21 SerCysAlaIleSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThr 40
Db 249 TCCTGTGACGCTCTGGATTCACTTTCAGTAGCTATACCATGTCTGGGTTCGCCGACT 308
Qy 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyIleThrTyrTyr 60

Db 309 CCGGAGAAAGGCTGTGAGTGGTGGCATCATTAAGTAGTGTTACTTACACTACTAT 368
Qy 61 LeuAspThrValIleGlyArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr 80
Db 369 CCAGACAGGTGTGAAGGGCCGATTCACCATCTCCAGAGACAAATGCCAAGAACCTCTGTAC 428
Qy 81 LeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArg----- 98
Db 429 CTGCAAAATGACCATGTGAAGTCTGAGGACACAGCATATTAAGTCTTCAAGAGATGAC 488
Qy 99 -----HisArgSerGlyTyrPheSerMetAspTyrTTPGlyGlnGlyThrSerValThr 116
Db 489 GGCTCCTACGGCTCTATTACTATGACTATGACTACTGGGGTCAAGAAACCTCAGTCACC 548
Qy 117 ValSerSer 119
Db 549 GTCTCTTCA 557

Search completed: June 3, 2006, 07:32:36
J0D time : 821.991 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 3, 2006, 06:56:49 ; Search time 13.5796 Seconds
(without alignments)
1548.108 Million cell updates/sec

Title: US-10-635-908-6
Perfect score: 617
Sequence: 1 DVKLVSQGGVLKGLSLKLT.....RSGYFSMDYWGQTSVTSS 119

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 246837 segs, 5886590 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/abs/NAISSWEB.spool/US10635908/runat_02062006_104226_10433/app_query.fasta.1
-DB=Published Applications NA-New -QFMT=fastap -SUFFIX=trpbn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs05h
-USRR=US10635908 -@CGN_1_1_26@runat_02062006_104226_10433 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLAG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -RCGAPOP=6 -RCGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA-New:*
1: /EMC_Celerra_SIDS3/prodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/prodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/prodata/2/pubpna/US07_NEW_PUB.seq:*
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6: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/prodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	476.5	77.2	1407	US-11-155-444-17	Sequence 17, Appl
2	452.5	73.3	2094	US-11-155-444-1	Sequence 1, Appl
3	452.5	73.3	2106	US-11-155-444-7	Sequence 7, Appl
4	452.5	73.3	2196	US-11-155-444-5	Sequence 5, Appl
5	452.5	73.3	2208	US-11-155-444-9	Sequence 9, Appl
6	440	71.3	873	US-11-154-103-27	Sequence 27, Appl
7	440	71.3	873	US-11-154-103-28	Sequence 28, Appl
8	437.5	70.9	870	US-11-154-103-30	Sequence 30, Appl
9	432	70.0	354	US-11-216-033-3	Sequence 3, Appl

10	431	69.9	357	7	US-11-300-563-23	Sequence 23, Appl
11	429.5	69.6	373	7	US-11-211-917-49	Sequence 49, Appl
12	429.5	69.6	373	7	US-11-211-917-95	Sequence 95, Appl
13	429.5	69.6	1410	7	US-11-211-917-53	Sequence 53, Appl
14	429	69.5	369	6	US-10-546-594-63	Sequence 63, Appl
15	429	69.5	369	6	US-10-546-594-69	Sequence 69, Appl
16	429	69.5	1419	6	US-10-546-594-129	Sequence 129, Appl
17	428.5	69.4	379	6	US-10-994-679-63	Sequence 63, Appl
18	427.5	69.3	362	7	US-11-023-959A-90	Sequence 90, Appl
19	425.5	69.0	366	7	US-11-254-679-37	Sequence 37, Appl
20	425	68.9	4027	7	US-11-169-140-1	Sequence 1, Appl
21	424.5	68.8	357	7	US-11-023-959A-185	Sequence 185, Appl
22	424	68.7	369	6	US-10-546-594-65	Sequence 65, Appl
23	423	68.6	732	6	US-10-503-433B-16	Sequence 16, Appl
24	423	68.6	803	6	US-10-503-433B-20	Sequence 20, Appl
25	422.5	68.5	345	7	US-11-023-959A-164	Sequence 164, Appl
26	422	68.4	351	7	US-11-254-679-65	Sequence 65, Appl
27	422	68.4	363	7	US-11-254-679-27	Sequence 27, Appl
28	422	68.4	801	6	US-10-503-433B-14	Sequence 14, Appl
29	421.5	68.3	357	7	US-11-023-959A-173	Sequence 173, Appl
30	421.5	68.3	360	7	US-11-254-679-8	Sequence 8, Appl
31	421	68.2	357	7	US-11-254-679-41	Sequence 41, Appl
32	419	67.9	741	7	US-11-216-033-5	Sequence 5, Appl
33	418	67.7	707	6	US-10-503-433B-19	Sequence 19, Appl
34	418	67.7	873	7	US-11-154-103-36	Sequence 36, Appl
35	417.5	67.7	357	7	US-11-023-959A-167	Sequence 167, Appl
36	417	67.6	357	7	US-11-254-679-61	Sequence 61, Appl
37	417	67.6	706	6	US-10-503-433B-17	Sequence 17, Appl
38	417	67.6	764	6	US-10-503-433B-11	Sequence 11, Appl
39	416	67.4	357	7	US-11-254-679-57	Sequence 57, Appl
40	416	67.4	363	7	US-11-254-679-12	Sequence 12, Appl
41	416	67.4	369	7	US-11-254-679-15	Sequence 15, Appl
42	416	67.4	704	6	US-10-503-433B-18	Sequence 18, Appl
43	416	67.4	873	6	US-11-154-103-35	Sequence 35, Appl
44	415.5	67.3	360	7	US-11-254-679-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-11-155-444-17
Sequence 17, Application US/11155444
Publication No. US20060104971A1
GENERAL INFORMATION:
APPLICANT: GABRIEL, ELLEN
APPLICANT: BROWNING, JEFFREY L.
TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
FILE REFERENCE: SIGNAL68CN
CURRENT APPLICATION NUMBER: US/11/155,444
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: PCT/US03/041393
PRIOR FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: 60/435,154
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/435,185
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 17
LENGTH: 1407
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: CBE11 pentameric
OTHER INFORMATION: heavy chain antibody construct
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1404)
US-11-155-444-17

Alignment Scores:

Pred. No.: 2,65e-54 Length: 1407
Score: 476.50 Matches: 92
Percent Similarity: 85.8% Conservative: 11
Best Local Similarity: 76.7% Mismatches: 16
Query Match: 77.2% Indels: 1
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-155-444-17 (1-1407)

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QY 1 AspValIyLeuValGluSerGlyGlyLeuValIyLeuGlyGlySerLeuYsleu 20
   1 GAGGTACAACTGCTGGAGTCTGGGGAGGCTTAGTAAGCCTGGAGGCTCCCTGAAACCTC 60
QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTyrValArgGlnThr 40
   61 TCCTGTGACGCTCTGGATTCACTTTCAGTGAATAATGATGATTTGGCTTGGCCAGACT 120
QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60
   121 CCGGAAAAGAGGCTGGAGTGGGTCCGACCAATTAGTGATGTGTATTACCTACTAT 180
QY 61 LeuAspThrValIyGlyArgPheThrIleSerArgAspAsnAlaIyAsnThrLeuTYr 80
   181 CCAGACAGGTGAAGGGGGGATTCAACCATCTCCAGAGACAAATGCCAAGAACCACTGTAC 240
QY 81 LeuGlnMetSerSerLeuYsSerGlyuAspThrAlaLeuPheTYrCyAlaArgHisArg 100
   241 CTGCAATATAGACGCTGAGTCTGAGACACAGCCATGTATTAATGTTAAGAGAGAG 300
QY 101 SerGly---TyrPheSerMetAspTYrTyrGlyGlnGlyThrSerValThrValSerSer 119
   301 AATGGTAACCTTTACTTACTTACTTACTGAGGCGCAAGGACCAAGGTACCGTCTCTCA 360
DB
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RESULT 2

US-11-155-444-1
Sequence 1, Application US/11155444
Publication No. US20060104971A1
GENERAL INFORMATION:
APPLICANT: GABER, ELLEN
APPLICANT: BAILLY, VERONIQUE
APPLICANT: BROWNING, JEFFREY L.
TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
FILE REFERENCE: BGN168CN
CURRENT APPLICATION NUMBER: US/11/155,444
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: PCT/US03/041393
PRIOR FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: 60/435,154
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/435,185
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 1
LENGTH: 2094
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of
OTHER INFORMATION: hucBE11/huBHA10 bispecific-1 antibody construct
US-11-155-444-1

Alignment Scores:

Pred. No.: 7,23e-51 Length: 2094
Score: 452.50 Matches: 87
Percent Similarity: 85.0% Conservative: 15
Best Local Similarity: 72.5% Mismatches: 17
Query Match: 73.3% Indels: 1
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-155-444-1 (1-2094)

QY 1 AspValIyLeuValGluSerGlyGlyLeuValIyLeuGlyGlySerLeuYsleu 20

DB 1 GAGGTACAACTGCTGGAGTCTGGGGAGGCTTAGTAAGCCTGGAGGCTCCCTGAGGCTC 60

QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTyrValArgGlnThr 40

DB 61 TCCTGTGACGCTCTGGATTCACTTTCAGTGAATAATGATGATTTGGCTTGGCCAGGCTC 120

QY 41 ProGluYsArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYrTYr 60

DB 121 CCGGAAAAGAGGCTGGAGTGGGTCCGACCAATTAGTGATGTGTATTACCTGCGCAAGAGAGAG 180

QY 61 LeuAspThrValIyGlyArgPheThrIleSerArgAspAsnAlaIyAsnThrLeuTYr 80

DB 181 CCAGACAGGTGAAGGGGGGATTCAACCATCTCCAGAGACAAATGCCAAGAACCACTGTAC 240

QY 81 LeuGlnMetSerSerLeuYsSerGlyuAspThrAlaLeuPheTYrCyAlaArgHisArg 100

DB 241 CTGCAATATAGACGCTGAGTCTGAGACACAGCCATGTATTAATGTTAAGAGAGAG 300

QY 101 SerGly---TyrPheSerMetAspTYrTyrGlyGlnGlyThrSerValThrValSerSer 119

DB 301 AATGGTAACCTTTACTTACTTACTTACTGAGGCGCAAGGACCAAGGTACCGTCTCTCA 360

RESULT 3

US-11-155-444-7
Sequence 7, Application US/11155444
Publication No. US20060104971A1
GENERAL INFORMATION:
APPLICANT: GABER, ELLEN
APPLICANT: BAILLY, VERONIQUE
APPLICANT: BROWNING, JEFFREY L.
TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
FILE REFERENCE: BGN168CN
CURRENT APPLICATION NUMBER: US/11/155,444
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: PCT/US03/041393
PRIOR FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: 60/435,154
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/435,185
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 7
LENGTH: 2106
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of
OTHER INFORMATION: hucBE11 monospecific-1 antibody construct
US-11-155-444-7

Alignment Scores:

Pred. No.: 7,29e-51 Length: 2106
Score: 452.50 Matches: 87
Percent Similarity: 85.0% Conservative: 15
Best Local Similarity: 72.5% Mismatches: 17
Query Match: 73.3% Indels: 1
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-155-444-7 (1-2106)

QY 1 AspValIyLeuValGluSerGlyGlyLeuValIyLeuGlyGlySerLeuYsleu 20

DB 1 GAGGTACAACTGCTGGAGTCTGGGGAGGCTTAGTAAGCCTGGAGGCTCCCTGAGGCTC 60

QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYrTYrMetSerTyrValArgGlnThr 40

DB 61 TCCTGTGACGCTCTGGATTCACTTTCAGTGAATAATGATGATTTGGCTTGGCCAGGCTC 120

Qy	41	ProGluIysAspGluLeuValAlaIleAsnSerAspGlyIleThrTyr	60
Db	121	CCGGAAAGGGGCTGGAGTGGTCCCAACCATTAGTAGTGTAAGTTACACTACCTACAT	180
Qy	61	LeuAspThrValIysGlyYArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr	80
Db	181	CCAGCACTGTGCAAGGGCGAGTTCAACATCTCCAGAGCAACATGCCAAGAACGCTCTAC	240
Qy	81	LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg	100
Db	241	CTGCAGATGACGACGCTGAGGCGCTGAGCAGACAGCGCTGTCTATTACTGCGCAGAGAGAG	300
Qy	101	SerGly---TyrPheSerMetAspTyrTrrTrrGlyGlnGlyThrSerValThrValSerSer	119
Db	301	AATGGTAACTTTTACTTACTTTGACTTACCTGGGGCCAGAGGACCAAGGTCAAGCTCTCTCA	360
RESULT 4			
US-11-155-444-5			
/ Sequence 5, Application US/11155444			
/ Publication No. US20060104971A1			
/ GENERAL INFORMATION:			
/ APPLICANT: GARBER, ELLEN			
/ APPLICANT: BAILLY, VERONIQUE			
/ APPLICANT: BROWNING, JEFFREY L.			
/ TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS, AND			
/ FILE REFERENCE: BGN168CN			
/ CURRENT APPLICATION NUMBER: US/11/155,444			
/ CURRENT FILING DATE: 2005-06-17			
/ PRIOR APPLICATION NUMBER: PCT/US03/041393			
/ PRIOR FILING DATE: 2003-12-22			
/ PRIOR APPLICATION NUMBER: 60/435,154			
/ PRIOR FILING DATE: 2002-12-20			
/ PRIOR APPLICATION NUMBER: 60/435,185			
/ PRIOR FILING DATE: 2002-12-20			
/ NUMBER OF SEQ ID NOS: 23			
/ SOFTWARE: PatentIn Ver. 3.3			
/ SEQ ID NO 5			
/ LENGTH: 2196			
/ TYPE: DNA			
/ ORGANISM: Artificial Sequence			
/ FEATURE:			
/ OTHER INFORMATION: Description of Artificial Sequence: hucBE11/huBH10			
/ OTHER INFORMATION: bispecific-2 antibody construct			
US-11-155-444-5			
Alignment Scores:			
Pred. No.:			
Score: 7,73e-51 Length: 2196			
Percent Similarity: 452.50 Matches: 87			
Best Local Similarity: 85.0% Conservative: 15			
Query Match: 72.5% Mismatches: 17			
Query Match: 73.3% Indels: 1			
DB: 7 Gaps: 1			
US-10-635-908-6 (1-119) x US-11-155-444-5 (1-2196)			
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Db	1	GAGTCAACACTGTGGAGTCTGGGGGAGCTTAGTGAAGCTGGAAGGTCCTCGAAGCTC	60
Qy	21	SerCysAlaIleAspGlyPheThrPheSerAsnTyrTyrMetSerTrrPValArgGlnThr	40
Db	61	TTCGTGCGACGCTCTGTGATTCACCTTTCAGTACTATTACATGTAATGGTTCGCCAGGCC	120
Qy	41	ProGluIysArgLeuGluLeuValAlaIleAsnSerArgGlyIleThrTyrTyr	60
Db	121	CCGGAAAGGGGCTGGAGTGGTCCCAACCATTAGTAGTGTAAGTTACACTACCTAT	180
Qy	61	LeuAspThrValIysGlyYArgPheThrIleSerArgAspAsnAlaIysAsnThrLeuTyr	80
Db	181	CCAGCACTGTGCAAGGGCGAGTTCAACATCTCCAGAGCAACATGCCAAGAACGCTCTAC	240
Qy	81	LeuGlnMetSerSerLeuIysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArg	100
Db	241	CTGCAGATGACGACGCTGAGGCGCTGAGCAGACAGCGCTGTCTATTACTGCGCAGAGAG	300
Qy	101	SerGly---TyrPheSerMetAspTyrTrrTrrGlyGlnGlyThrSerValThrValSerSer	119
Db	301	AATGGTAACTTTTACTTACTTTGACTTACCTGGGGCCAGAGGACCAAGGTCAAGCTCTCTCA	360

[illegible]

FEATURE:
OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-30

Alignment Scores:
Pred. No.: 2,11e-49 Length: 870
Score: 437.50 Matches: 87
Percent Similarity: 85.7% Conservative: 15
Best Local Similarity: 73.1% Mismatches: 14
Query Match: 70.9% Indels: 3
DB: 7 Gaps: 2

US-10-635-908-6 (1-119) x US-11-154-103-30 (1-870)

QY 2 VallyLeuValGluSerGlyGlyGlyLeuValVlyLeuGlySerLeuLysLeuSer 21
DB 70 GTGCACTCGAGAGTGGGGGAGGCTGTGTCAAGCTGGGGGTCCTGAGACTCTCC 129
QY 22 CyAlaAlaSerGlyPheThrPheSerAsnTrpTyrMetSerTrpValArgGlnThrPro 41
DB 130 TGTGCAGCCTCTGATTCACCTTTAGTACTATTGGATGAGTGGGTCCGCGCAGGCTCCA 189
QY 42 GluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTrpTyrLeu 61
DB 190 GGAAGGGGCTGAGTGGGTGCGCCAACTAAACCGCGATGAAAGTGCACGCTATTATGTG 249
QY 62 AspThrVallyLeuGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrLeu 81
DB 250 GACTGTGTGAAGGCGCCATTCCACCATCTCCAGAGACAGCCCAAGAACTCACTGATCTG 309
QY 82 GlMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArgSer 101
DB 310 CAATGACACGCTGAGAGCGGAGACACGCGTGTGATTACTGTGAGAGATCGGGCG 369
QY 102 ---GlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 370 GTGGGGGACTTC-----GATCTCTGGGGCGTGGCACCTGTGACCGTCTCTCTCA 420

RESULT 9

US-11-216-033-3

Sequence 3, Application US/11216033
Publication No. US20060104899A1

GENERAL INFORMATION:

APPLICANT: HANSEN, HANS J.

APPLICANT: GRIFETHS, GARY L.

APPLICANT: MCBRIDE, WILLIAM J.

APPLICANT: LEBUNG, SHUI-ON

APPLICANT: QU, ZHENGGXING

TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR

FILE REFERENCE: 40923-0074US4

CURRENT APPLICATION NUMBER: US/11/216,033

PRIOR FILING DATE: 2005-09-01

PRIOR APPLICATION NUMBER: US/09/823,746

PRIOR FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: 09/337,756

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patent In Ver. 3.3

SEQ ID NO 3

LENGTH: 354

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: NAME/KEY: CDS

LOCATION: (1)..(354)

OTHER INFORMATION: Description of Artificial Sequence: Synthetic 679 Vn

US-11-216-033-3

Alignment Scores:

Pred. No.: 3.25e-49 Length: 354

Score: 432.00 Matches: 86
Percent Similarity: 82.2% Conservative: 11
Best Local Similarity: 72.9% Mismatches: 21
Query Match: 70.0% Indels: 0
DB: 7 Gaps: 0

US-10-635-908-6 (1-119) x US-11-216-033-3 (1-354)

QY 2 VallyLeuValGluSerGlyGlyGlyLeuValVlyLeuGlySerLeuLysLeuSer 21
DB 1 GTCCAACTCGAGAGTGGGGGAGACTTATGAGAGCTGAGAGGCTCTGAAACTCTCC 60
QY 22 CyAlaAlaSerGlyPheThrPheSerAsnTrpTyrMetSerTrpValArgGlnThrPro 41
DB 61 TGTGCAGCCTCTGATTCACCTTTAGTACTATTGGATGAGTGGGTCCGCGCAGGCTCCA 120
QY 42 GluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTrpTyrLeu 61
DB 121 GAAAGAGGCTGAGTGGGTGCGCCAACTAAACCGCGATGAAAGTGCACGCTATTATGTG 180
QY 62 AspThrVallyLeuGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrLeu 81
DB 181 GACAGTGTGAAGGCTGATTCACCATCTCCAGAGACAAATGCCAAGAACTATATCTG 240
QY 82 GlMetSerSerLeuLysSerGluAspThrAlaLeuPheTyrCysAlaArgHisArgSer 101
DB 241 CAATGACACGCTGAGAGCGGAGACACGCGTGTGATTACTGTGAGAGATCGGGCG 300
QY 102 GlyTyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 119
DB 301 GGGGACTGGGACTTCGATGTCTGGGGCCAGGAGCAACGCTCTCCGCTCTCTCA 354

RESULT 10

US-11-300-563-23

Sequence 23, Application US/11300563
Publication No. US20060088526A1

GENERAL INFORMATION:

APPLICANT: BOLT, SARAH L.

APPLICANT: CLARK, MICHAEL R.

APPLICANT: GORMAN, SCOTT D.

APPLICANT: ROUTLEDGE, EDWARD G.

APPLICANT: WALDMANN, HERMAN

TITLE OF INVENTION: HUMANIZED ANTI-CD3 SPECIFIC ANTIBODIES (AS AMENDED)

FILE REFERENCE: 604-704

CURRENT APPLICATION NUMBER: US/11/300,563

PRIOR FILING DATE: 2005-12-15

PRIOR APPLICATION NUMBER: 10/743,423

PRIOR FILING DATE: 2003-12-23

PRIOR APPLICATION NUMBER: 08/478,684

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 9206422.9

PRIOR FILING DATE: 1992-03-24

PRIOR APPLICATION NUMBER: PCT/GB92/01933

PRIOR FILING DATE: 1992-10-21

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 23

LENGTH: 357

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: NAME/KEY: CDS

LOCATION: (1)..(357)

OTHER INFORMATION: Description of Artificial Sequence: Synthetic nucleotide

US-11-300-563-23

Alignment Scores:

Pred. No.: 4.47e-49 Length: 357

Score: 431.00 Matches: 82

Percent Similarity: 84.9% Conservative: 19

Best Local Similarity: 68.9% Mismatches: 18

Query Match: 69.9% Indels: 0

DB: 7 Gaps: 0

US-10-635-908-6 (1-119) x US-11-300-563-23 (1-357)

QY 1 AspVallyLeuValGluSerGlyGlyGlyLeuVallyLeuGlyGlySerLeuysLeu 20
Db 1 GAGGTCCAACTGCTGGAGTCTGGGGCGGCTTTAGTGCACAGCTGGAGGGTCCCTGAGACTC 60

QY 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTYRtyrMetSerTrpValArgIntr 40
Db 61 TCTGTGGCAGCTCAGGATTCACCTTTCAGTAGCTTCCAAATGGCCGCTCCGCCAGGCT 120

QY 41 ProGluValArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYRtyr 60
Db 121 CAGGGAAGGCTGTGAGTGGGTCTTCAACCACTTAGTACAGTGTGTGAAGTACTTACT 180

QY 61 LeuAspThrVallyArgPheThrIleSerAspAsnAlaIysAsnThrLeuTYR 80
Db 181 CGAGACTCCGTGAAGGGCGGATTCACCTATCTCAGAGATAATAGCAAAATACCTATAC 240

QY 81 LeuGlnMetSerSerLeuysSerGlyuAspThrAlaLeuPheTYRCyAlaArgHisArg 100
Db 241 CTGCAGAAATGAATAGTCTGAGGCTGAGACACGGCGCTATTACTGTCCAAATTTCCG 300

QY 101 SerGlyTYRPheserMetAspTYRTPGlyGlnGlyThrSerValThrValSerSer 119
Db 301 CAGTACAGTGTGCTTGTATTACTGGGGCCAAAGGACCTGTCTCAGCTTCTCTCA 357

RESULT 11

US-11-211-917-49

/ Sequence 49, Application US/11211917

/ Publication No. US20060093600A1

/ GENERAL INFORMATION:

/ APPLICANT: BEDIAN, VAHE

/ APPLICANT: GLADUE, RONALD P.

/ APPLICANT: CORVALAN, JOSE

/ APPLICANT: JIA, XIAO-CHI

/ APPLICANT: FENG, XIAO

/ TITLE OF INVENTION: ANTIBODIES TO CD40

/ FILE REFERENCE: ABX-PF/3 US

/ CURRENT APPLICATION NUMBER: US/11/211,917

/ PRIOR FILING DATE: 2005-08-25

/ PRIOR APPLICATION NUMBER: US/10/292,088

/ PRIOR FILING DATE: 2002-11-08

/ PRIOR APPLICATION NUMBER: 60/348,980

/ PRIOR FILING DATE: 2001-11-09

/ NUMBER OF SEQ ID NOS: 147

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 49

/ LENGTH: 373

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-11-211-917-49

Alignment Scores:

Pred. No.: 7,52e-49 Length: 373

Score: 429.50 Matches: 85

Percent Similarity: 80.5% Conservative: 14

Best Local Similarity: 69.1% Mismatches: 19

Query Match: 69.6% Indels: 5

DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-211-917-49 (1-373)

QY 2 VallyLeuValGluSerGlyGlyGlyLeuVallyLeuGlyGlySerLeuysLeuSer 21
Db 4 GTGCACCTGCTGAGTCTGGGGAGGCGTGTCCAGCTGCAGCTCCCTGAGACTCTCC 63

QY 22 CyAlaAlaSerGlyPheThrPheSerAsnTYRtyrMetSerTrpValArgIntrPro 41
Db 64 TGTGCAGCTCTGATTCACCTTCAAGTCCGTATGCGACACTGGGTCGCCAGGCTCCA 123

QY 42 GluLYArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYRtyrLeu 61
Db 124 GCGAAGGGCTGAGTGGGTGCGAGCTTATCATCTGATGAGGTAAATTAATCTATCCA 183

QY 62 AspThrVallyArgPheThrIleSerArgAsnAlaIysAsnThrLeuTYRleu 81
Db 184 GACTCCGGAAGGGCGGATTCACTTCACAGAGCAAAATTCMAAAGCGCTGATCTG 243

QY 82 GlnMetSerSerLeuysSerGlyuAspThrAlaLeuPheTYRCyAlaArgHisArgSer 101
Db 244 CAAATGAACAGCTGAGAGCTGAGGACAGGCTGTGTATTACTGTACAGAGAGAGGACT 303

QY 102 Gly-----TYRPheserMetAspTYRTPGlyGlnGlyThrSerValThr 116
Db 304 GGAAGACTTACTACCACTAGTGTGATGACGCTGGGCGCAAGGACACAGGTACCC 363

QY 117 ValSerSer 119
Db 364 GTCTCTCCA 372

RESULT 12

US-11-211-917-95

/ Sequence 95, Application US/11211917

/ Publication No. US20060093600A1

/ GENERAL INFORMATION:

/ APPLICANT: BEDIAN, VAHE

/ APPLICANT: GLADUE, RONALD P.

/ APPLICANT: CORVALAN, JOSE

/ APPLICANT: JIA, XIAO-CHI

/ APPLICANT: FENG, XIAO

/ TITLE OF INVENTION: ANTIBODIES TO CD40

/ FILE REFERENCE: ABX-PF/3 US

/ CURRENT APPLICATION NUMBER: US/11/211,917

/ PRIOR FILING DATE: 2005-08-25

/ PRIOR APPLICATION NUMBER: US/10/292,088

/ PRIOR FILING DATE: 2002-11-08

/ PRIOR APPLICATION NUMBER: 60/348,980

/ PRIOR FILING DATE: 2001-11-09

/ NUMBER OF SEQ ID NOS: 147

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 95

/ LENGTH: 373

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-11-211-917-95

Alignment Scores:

Pred. No.: 7,52e-49 Length: 373

Score: 429.50 Matches: 85

Percent Similarity: 80.5% Conservative: 14

Best Local Similarity: 69.1% Mismatches: 19

Query Match: 69.6% Indels: 5

DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-211-917-95 (1-373)

QY 2 VallyLeuValGluSerGlyGlyGlyLeuVallyLeuGlyGlySerLeuysLeuSer 21
Db 4 GTGCACCTGCTGAGTCTGGGGAGGCGTGTCCAGCTGCAGCTCCCTGAGACTCTCC 63

QY 22 CyAlaAlaSerGlyPheThrPheSerAsnTYRtyrMetSerTrpValArgIntrPro 41
Db 64 TGTGCAGCTCTGATTCACCTTCAAGTCCGTATGCGACACTGGGTCGCCAGGCTCCA 123

QY 42 GluLYArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTYRtyrLeu 61
Db 124 GCGAAGGGCTGAGTGGGTGCGAGCTTATCATCTGATGAGGTAAATTAATCTATCCA 183

QY 62 AspThrVallyArgPheThrIleSerArgAsnAlaIysAsnThrLeuTYRleu 81
Db 184 GACTCCGTAAGGGCGGATTCACTTCACAGAGCAAAATTCMAAAGCGCTGATCTG 243

QY 82 GlnMetSerSerLeuysSerGlyuAspThrAlaLeuPheTYRCyAlaArgHisArgSer 101
Db 244 CAAATGAACAGCTGAGAGCTGAGGACAGGCTGTGTATTACTGTACAGAGAGAGGACT 303

OY 102 G1Y-----TyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThr 116
|||
Db 304 GGAAGACTTACTACACACTACCGCGGTATGAGCTGTGGGCGCAAGGACCAACGCTCACC 363
|||
OY 117 ValSerSer 119
|||
Db 364 GTCTCCTCA 372
|||

RESULT 13

US-11-211-917-53
/ Sequence 53, Application US/11211917
/ Publication No. US20060093600A1
/ GENERAL INFORMATION:
/ APPLICANT: BEDIAN, VAHE
/ APPLICANT: GLADIE, RONALD P.
/ APPLICANT: CORVALAN, JOSE
/ APPLICANT: JIA, XIAO-CHI
/ APPLICANT: FENG, XIAO
/ TITLE OF INVENTION: ANTIBODIES TO CD40
/ FILE REFERENCE: ABX-PF/3 US
/ CURRENT APPLICATION NUMBER: US/11/211,917
/ PRIOR FILING DATE: 2005-08-25
/ PRIOR APPLICATION NUMBER: US/10/292,088
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: 60/348,980
/ PRIOR FILING DATE: 2001-11-09
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 53
/ LENGTH: 1410
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-211-917-53

Alignment Scores:
Pred. No.: 4,81e-48 Length: 1410
Score: 429.50 Matches: 85
Percent Similarity: 80.5% Conservative: 14
Best Local Similarity: 69.1% Mismatches: 19
Query Match: 69.6% Indels: 5
DB: 7 Gaps: 1

US-10-635-908-6 (1-119) x US-11-211-917-53 (1-1410)

OY 2 VallyLeuValGluSerGlyGlyGlyLeuVallyLeuGlySerLeuLeuSer 21
|||
Db 61 GTGCACTGTGAGTGTGGGGAGGCGCTGCTCAGCGCTGGAGGTCCTCGAAGCTCTCC 120
|||
OY 22 CysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThrPro 41
|||
Db 121 TGTGCACTGTGAGTGTGGGGAGGCGCTGCTCAGCGCTGATGCACTGGGTCCTCGAAGCTCTCC 180
|||
OY 42 GluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyrLeu 61
|||
Db 181 GGCAGAGGGCGTGGAGTGGGCGAGTTATATCATCTATGAGGTAAATAAATACTATGCA 240
|||
OY 62 AspThrVallyLeuGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrLeu 81
|||
Db 241 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGCAAGCGCTATCTG 300
|||
OY 82 GlnMetSerSerLeuLysSerGlyAspThrAlaLeuPheTyrCysAlaArgHisArgSer 101
|||
Db 301 CAATGAAGACCTGAGAGGCTGAGAGACACGGCTGTGATTACTGTACGAGAGAGGAGCT 360
|||
OY 102 G1Y-----TyrPheSerMetAspTyrTrpGlyGlnGlyThrSerValThr 116
|||
Db 361 GGAAGACTTACTACACACTACTGTGTATGAGCGTGTGGGCGCAAGGACCAACGCTCACC 420
|||
OY 117 ValSerSer 119
|||
Db 421 GTCTCCTCA 429
|||

RESULT 14

US-10-546-594-63
/ Sequence 63, Application US/10546594
/ Publication No. US20060088538A1
/ GENERAL INFORMATION:
/ APPLICANT: HOSOKAWA, Saiko
/ APPLICANT: AOKI, Masahiko
/ APPLICANT: HIRAKAWA, Yoko
/ APPLICANT: ITAMI, Selma
/ APPLICANT: UMEKI, Hiroe
/ APPLICANT: SAIKAWA, Yoshiro
/ APPLICANT: KUMAI, Koichiro
/ APPLICANT: FUKUDA, Kazumasa
/ TITLE OF INVENTION: MONOCLONAL ANTIBODY AND GENE ENCODING THE SAME, HYBRIDOMA, PHARM.

/ FILE REFERENCE: 238067
/ CURRENT APPLICATION NUMBER: US/10/546,594
/ PRIOR FILING DATE: 2005-08-19
/ PRIOR APPLICATION NUMBER: JP 2003/54670
/ PRIOR FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: JP 2003/194643
/ PRIOR FILING DATE: 2003-07-09
/ NUMBER OF SEQ ID NOS: 132
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 63
/ LENGTH: 369
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(369)
/ OTHER INFORMATION:
US-10-546-594-63

Alignment Scores:
Pred. No.: 8,63e-49 Length: 369
Score: 429.00 Matches: 85
Percent Similarity: 81.3% Conservative: 15
Best Local Similarity: 69.1% Mismatches: 19
Query Match: 69.5% Indels: 4
DB: 6 Gaps: 1

US-10-635-908-6 (1-119) x US-10-546-594-63 (1-369)

OY 1 AspVallyLeuValGluSerGlyGlyGlyLeuVallyLeuGlySerLeuLeuSer 20
|||
Db 1 GAGTGCAGCTGTGAGTGTGGGGAGGCGCTGCTCAGCGCTGGAGGTCCTCGAAGCTC 60
|||
OY 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTyrMetSerTrpValArgGlnThrPro 40
|||
Db 61 TCTGTGCACTGTGAGTGTGGGGAGGCGCTGCTCAGCGCTGATGCACTGGGTCCTCGAAGCTCTCC 120
|||
OY 41 ProGluLysArgLeuGluLeuValAlaAlaIleAsnSerAspGlyGlyIleThrTyrTyrLeu 60
|||
Db 121 CCAGCAAGAGGGCGTGGAGTGGGCGAGTTATATCATCTATGAGGTAAATAAATACTATGCA 180
|||
OY 61 LeuAspThrVallyLeuGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrLeu 80
|||
Db 181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGCAAGCGCTATCTG 240
|||
OY 81 LeuGlnMetSerSerLeuLysSerGlyAspThrAlaLeuPheTyrCysAlaArgHisArgSer 100
|||
Db 241 CTGCAATGAAGACCTGAGAGGCTGAGAGACACGGCTGTGATTACTGTACGAGAGAGGAGCT 300
|||
OY 101 SerG1Y-----PheSerMetAspTyrTrpGlyGlnGlyThrSerValThr 116
|||
Db 301 CACTCCAGCATTTTGTGAGTGGTCCCTTGACTGACTGAGGCGGACACCGCTGCTCACC 360
|||
OY 117 ValSerSer 119
|||
Db 361 GTCTCCTCA 369
|||

RESULT 15

US-10-546-594-69

```
; Sequence 69, Application US/10546594
; Publication No. US2006008538A1
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: AOKI, Masahiko
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITAMI, Seima
; APPLICANT: UMEKI, Hiroe
; APPLICANT: SAIKAWA, Yoshitro
; APPLICANT: KUMAI, Koichiro
; APPLICANT: FUKUDA, Kazumasa
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND GENE ENCODING THE SAME, HYBRIDOMA, PHARMA
; FILE REFERENCE: 238067
; CURRENT APPLICATION NUMBER: US/10/546,594
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: JP 2003/54670
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: JP 2003/194643
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(369)
; OTHER INFORMATION:
US-10-546-594-69
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Alignment Scores:
Pred. No.: 8,63e-49 Length: 369
Score: 429.00 Matches: 85
Percent Similarity: 81.3% Conservative: 15
Best Local Similarity: 69.1% Mismatches: 19
Query Match: 69.5% Indels: 4
DB: 6 Gaps: 1
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US-10-635-908-6 (1-119) x US-10-546-594-69 (1-369)

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QY 1 AapvAllyLeuValIuSerGlyGlyLeuValLyLeuGlyGlySerLeuYsleu 20
Db 1 GAGGTGACCTGCTGGAGCTGGGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 60
QY 21 SerCyAlAlAserGlyPheThrPheSerAsnTyTrMetSerTyPValArgGlnThr 40
Db 61 TCCTGCGACCTCTGATTCACCTTCAGTACGCTATGCTACGCTGCGCAGGCT 120
QY 41 ProGluYsArgLeuGluLeuValAlAlAlIleAsnSerAspGlyGlyIleThrTyTr 60
Db 121 CCAGGCAAGGCTGAGTGGTGGCAGTATATCATATGATGAGCAATAATATCTAC 180
QY 61 LeuAspThrValLyGlyArgPheThrIleSerArgAspAsnAlaYsAsnThrLeuTy 80
Db 181 GCGACTCCGTAAGGCGCATTCACCATTCAGAGACATTCAGAGACACCTGTAT 240
QY 81 LeuGlnMetSerSerLeuYsSerGluAspThrAlaLeuPheTyTrCysAlaArgHisArg 100
Db 241 CTCGAATGACAGCTGAGAGCTGAGAGACAGAGCTGTGTATCTGTGCGAGATCG 300
QY 101 SerGlyTyTr-----PheSerMetAspTyTrTyrGlyGlnGlyThrSerValThr 116
Db 301 CACTCCCTACGATTTTGGAGTGGTCTTACTGACTACTGCGGCAAGGAACTGTGAC 360
QY 117 ValSerSer 119
Db 361 GTCTCTCA 369
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 3, 2006, 03:53:44 ; Search time 6305.61 Seconds
(without alignments)
3255.375 Million cell updates/sec

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Perfect score: 1116
Sequence: 1 DIVMTQSGRFMTSTVGDVRS.....EVTHTGLSSPVTKSFNRGEC 214

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 segs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFRTX=rge -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h
-USER=US10635908.@CCN_1_1_5767 @runat_02062006_104214_10235 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_srs:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1030	92.3	717 2	AX556961 Sequence
2	1030	92.3	717 2	AX709560 Sequence
3	1017	91.1	714 2	AR116649 Sequence

4	1017	91.1	714 2	BD069191	BD069191 Antibody
5	1017	91.1	714 2	CQ902834	CQ902834 Sequence
6	1017	91.1	714 2	AR233008	AR233008 Sequence
7	1017	91.1	714 2	AR237939	AR237939 Sequence
8	1017	91.1	714 2	169460	169460 Sequence 27
9	1017	91.1	714 2	173079	173079 Sequence 27
10	1017	91.1	714 2	179264	179264 Sequence 27
11	1017	91.1	714 2	187038	187038 Sequence 27
12	1017	91.1	714 2	AR647560	AR647560 Sequence
13	1007	90.2	1501 2	CS239095	CS239095 Sequence
14	977.5	87.6	699 2	CS133169	CS133169 Sequence
15	962	86.2	4604 8	AR852004	AR852004 Synthetic
16	956	85.7	702 2	AX829027	AX829027 Sequence
17	954.5	85.5	711 2	DD163548	DD163548 AN ANTIBO
18	951	85.2	642 5	AB004304	AB004304 Homo sapi
19	948	84.9	642 5	AX329190	AX329190 Sequence
20	948	84.9	807 5	AB064078	AB064078 Homo sapi
21	945	84.7	748 2	AR566365	AR566365 Sequence
22	945	84.7	12190 2	CS101405	CS101405 Sequence
23	944	84.6	642 2	CS027619	CS027619 Sequence
24	943	84.5	660 2	AR139116	AR139116 Sequence
25	943	84.5	660 2	AR237916	AR237916 Sequence
26	942	84.4	793 5	AB064140	AB064140 Homo sapi
27	942	84.4	812 5	AB064043	AB064043 Homo sapi
28	942	84.4	812 5	AB064045	AB064045 Homo sapi
29	939.5	84.2	928 2	AX251598	AX251598 Sequence
30	939	84.1	2073 2	CQ904166	CQ904166 Sequence
31	939	84.1	2082 2	CQ904163	CQ904163 Sequence
32	937	84.0	759 5	AB064052	AB064052 Homo sapi
33	937	84.0	813 5	AB064081	AB064081 Homo sapi
34	936	83.9	642 5	AB027444	AB027444 Homo sapi
35	936	83.9	974 2	BD131246	BD131246 Human mon
36	936	83.9	974 2	AR589372	AR589372 Sequence
37	936	83.9	974 2	AX305000	AX305000 Sequence
38	936	83.9	974 2	AX306529	AX306529 Sequence
39	935	83.8	2193 2	CQ904169	CQ904169 Sequence
40	935	83.8	2196 2	CQ904172	CQ904172 Sequence
41	935	83.8	2166 2	CQ904175	CQ904175 Sequence
42	935	83.8	5387 2	CQ904180	CQ904180 Sequence
43	935	83.8	6620 2	CQ904178	CQ904178 Sequence
44	935	83.8	7060 2	CQ904157	CQ904157 Sequence
45	935	83.8	7171 2	CQ904160	CQ904160 Sequence

ALIGNMENTS

RESULT 1
AX556961
LOCUS AX556961 717 bp DNA
DEFINITION Sequence 16 from Patent WO02060955.
ACCESSION AX556961
VERSION AX556961.1 GI:25900019

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .717
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Humanized C5E10 Light Chain Sequence"

ORIGIN

Alignment Scores:
Pred. No.: 6.08e-115 Length: 717
Score: 1030.00 Matches: 198
Percent Similarity: 96.7% Conservative: 9

Best Local Similarity: 92.5% Mismatches: 7
Query Match: 92.3% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AX556961 (1-717)

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QY 1 AaplleValMetThrcInserGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 73 GACATTGTGATATTCACAGTCTCAAAATTCATGTCCACATCAGTAGAAGAGGCTCAAC 132
QY 21 IleThrCysLeuAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 133 ATCACCCTGCAAGCCAGTCAGATGTGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
QY 41 GlyGlnSerProIleuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 193 GGACATCTCTCAACTACTGATTTACTGTCTATCCACCCGGACACTGGAGTCCCTGAT 252
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 253 CGCTTCACAGGCGAGTGGATCTGGACAGATTCTACCTCCATTCAGCAATGTGCACTCT 312
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
DB 313 GAAGACTTGGCAGATTAATTTCTCTCAGTTATATAGACGATCTCTCAGCTTCGAGGG 372
QY 101 GlyThrIleLeuGlnIleIleValArgThrValAlaAlaProSerValPheIlePhePro 120
DB 373 GGAGCAAGCTGGAATTCACAGTACGTCGTCGACCACTGTCTTCACTTCCGCCCA 432
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 433 TCTGATGACAGATGTGAATCTGGAACCTCTGTTGTGCTGTGTAATTAATCTTCTAT 492
QY 141 ProArgGlnAlaIleValGlnTyrPlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 493 CCAGAGAGCCCAAAGTACAGTGAAGTGGATTAACCCCTCCAAATCGGGTAACTCCAG 552
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 553 GAGAGTGTCAAGAGCAGCAGCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 612
QY 181 LeuSerLeuAlaAspTyrGlnIleValIleValTyrAlaCysGluValThrIleGlnGly 200
DB 613 CTGAGCAAAAGCAGATCAAGAAACCAAAAGTCTAGCCCTGCGAAGTCAACCATCAGGGC 672
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB 673 CTGAGCTCGCCCTCAAAAGACTTCAACAGGGGAGAGTGT 714
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RESULT 2
AX709560 717 bp DNA linear PAT 04-APR-2003
LOCUS Sequence 16 from Patent WO02096948.
DEFINITION AX709560
ACCESSION AX709560
VERSION AX709560.1 GI:29564980
KEYWORDS
ORGANISM
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Brajlawsky,G.R., Hanna,N., Chinn,P. and Hariharan,K.
TITLE Engineered tetraivalent antibodies and methods of use
JOURNAL Patent: WO 02096948-A 16 05-DEC-2002;
Idex Pharmaceuticals Corporation (US)
Location/Qualifiers

FEATURES
source 1..717
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic nucleotide sequence of CSE10 light chain"

ORIGIN

Alignment Scores:
Pred. No.: 6.08e-115 Length: 717
Score: 1030.00 Matches: 198
Percent Similarity: 96.7% Conservative: 9
Best Local Similarity: 92.5% Mismatches: 7
Query Match: 92.3% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AX709560 (1-717)

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QY 1 AaplleValMetThrcInserGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 73 GACATTGTGATATTCACAGTCTCAAAATTCATGTCCACATCAGTAGAAGAGGCTCAAC 132
QY 21 IleThrCysLeuAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 133 ATCACCCTGCAAGCCAGTCAGATGTGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
QY 41 GlyGlnSerProIleuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 193 GGACATCTCTCAACTACTGATTTACTGTCTATCCACCCGGACACTGGAGTCCCTGAT 252
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 253 CGCTTCACAGGCGAGTGGATCTGGACAGATTCTACCTCCATTCAGCAATGTGCACTCT 312
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
DB 313 GAAGACTTGGCAGATTAATTTCTCTCAGTTATATAGACGATCTCTCAGCTTCGAGGG 372
QY 101 GlyThrIleLeuGlnIleIleValArgThrValAlaAlaProSerValPheIlePhePro 120
DB 373 GGAGCAAGCTGGAATTCACAGTACGTCGTCGACCACTGTCTTCACTTCCGCCCA 432
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 433 TCTGATGACAGATGTGAATCTGGAACCTCTGTTGTGCTGTGTAATTAATCTTCTAT 492
QY 141 ProArgGlnAlaIleValGlnTyrPlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 493 CCAGAGAGCCCAAAGTACAGTGAAGTGGATTAACCCCTCCAAATCGGGTAACTCCAG 552
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 553 GAGAGTGTCAAGAGCAGCAGCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 612
QY 181 LeuSerLeuAlaAspTyrGlnIleValIleValTyrAlaCysGluValThrIleGlnGly 200
DB 613 CTGAGCAAAAGCAGATCAAGAAACCAAAAGTCTAGCCCTGCGAAGTCAACCATCAGGGC 672
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB 673 CTGAGCTCGCCCTCAAAAGACTTCAACAGGGGAGAGTGT 714
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RESULT 3
AR116649 714 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 24 from patent US 6133426.
DEFINITION AR116649
ACCESSION AR116649
VERSION AR116649.1 GI:14096971
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
Unclassified.

REFERENCE
AUTHORS Gonzalez,T.N., Leon,G.S.R. and Presta,L.G.
TITLE Humanized anti-IL-8 monoclonal antibodies
JOURNAL Patent: US 6133426-A 24 17-OCT-2000;
Location/Qualifiers

FEATURES
source 1..714
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 2,29e-113 Length: 714
 Score: 1017.00 Matches: 194
 Percent Similarity: 96.3% Conservative: 12
 Best Local Similarity: 90.7% Mismatches: 8
 Query Match: 91.1% Indels: 0
 DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AB116649 (1-714)

QY 1 AspIleValMetThGlnSerGlnArgPheMetSerThrThValGlyAspArgValSer 20
 DB 70 GATATCGTCATGACACAGCTCAAAATTCATGTCACATGAGAGACGGGTCAAC 129
 QY 21 IletHrCyAlaAlaSerGlnAsnValValSerAlaValAlaTPrTgGlnGlnLysPro 40
 DB 130 GTCACTGCAAGCCGACGATGAGATGCTGATGATGATGATGATGATGATGATGAT 189
 QY 41 GlyGlnSerProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
 DB 190 GGGCAATCTCTCAAGACATGATTTCTGTCATCTTACCGGTACAGTGGAGTCCCTGAT 249
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
 DB 250 CGCTTCACAGGACGATGATCTGGACAGATTCATCTCACCATCAGCATGTCAGTCT 309
 QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTPrThrPheGlyGly 100
 DB 310 GAAAGCTTGCAAGATTTCTGTCAGCAATATACATCTATCTCTCTCTCTCTCTCTCT 369
 QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
 DB 370 GGGACCAAGCTGAGCTTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
 QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
 DB 430 TCTGATGACAGATGTAATCTGGAATCTGCTTCTGTTGTGCTGCTGCTGCTGCTGCTGCT 489
 QY 141 ProArgGlnAlaLysValGlnTPrLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
 DB 490 CCCAGAGAGGCCAAAGTACAGTGAAGGTGATACGCCCTCCAAATCGGGTAACTCCAG 549
 QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
 DB 550 GAGAGGTGTCAAGAGCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 609
 QY 181 LeuSerLysAlaAspTyrGlnLysValTyrAlaCysGlnValThrIleGlnGly 200
 DB 610 CTGAGCAAGCAGACATCAAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGGC 669
 QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlnLys 214
 DB 670 CTGAGCTCGCCGCTCAACAAAGACCTTCACAGGAGGAGGTGT 711
 RESULT 4
 BD069191 714 bp DNA linear PAT 27-AUG-2002
 LOCUS BD069191 Antibody fragment-polymer conjugates and humanized anti-IL-8
 DEFINITION monoclomal antibodies.
 ACCESSION BD069191.1 GI:22614794
 VERSION JP 2001512489-A/25.
 KEYWORDS unidentifed
 SOURCE unidentifed
 ORGANISM unclassified sequences.
 REFERENCE 1 (bases 1 to 714)
 AUTHORS Hseil,V., Koumenis,I., Leong,S.R., Presta,L.G., Shahrokh,Z. and Zapata,G.A.
 TITLE Antibody fragment-polymer conjugates and humanized anti-IL-8
 JOURNAL monoclomal antibodies
 GENETECH INC Patent: JP 2001512489-A 25 21-AUG-2001;

COMMENT

OS Unidentified
 PN JP 2001512489-A/25
 PD 21-AUG-2001
 PF 20-FEB-1998 JP 1998536905
 PR 21-FEB-1997 US 08/804444, 22-JAN-1998 US 09/012116 PI
 VANESSA HSEIL,IPHIGENIA KOUMENIS,STEVEN R LEONG,LEONARD G PI
 PRESTA,
 PI ZAHRA SHAHROKH,GERARDO A ZAPATA
 PC C12N15/13,C07K19/00,A61K47/48,C07K16/24,C12N15/85,C12N5/10 CC
 Strandedness: Double;
 CC Topology: Linear;
 CC Antibody fragment-polymer conjugates and humanized anti-IL-8
 CC monoclonal
 CC antidiodes
 CC Key
 FT source location/Qualifiers
 FT 1..714 location/Qualifiers
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN

Alignment Scores:
 Pred. No.: 2,29e-113 Length: 714
 Score: 1017.00 Matches: 194
 Percent Similarity: 96.3% Conservative: 12
 Best Local Similarity: 90.7% Mismatches: 8
 Query Match: 91.1% Indels: 0
 DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x BD069191 (1-714)

QY 1 AspIleValMetThGlnSerGlnArgPheMetSerThrThValGlyAspArgValSer 20
 DB 70 GATATCGTCATGACACAGCTCAAAATTCATGTCACATGAGAGACGGGTCAAC 129
 QY 21 IletHrCyAlaAlaSerGlnAsnValValSerAlaValAlaTPrTgGlnGlnLysPro 40
 DB 130 GTCACTGCAAGCCGACGATGAGATGCTGATGATGATGATGATGATGATGATGATGAT 189
 QY 41 GlyGlnSerProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
 DB 190 GGGCAATCTCTCAAGACATGATTTCTGTCATCTTACCGGTACAGTGGAGTCCCTGAT 249
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
 DB 250 CGCTTCACAGGACGATGATCTGGACAGATTCATCTCACCATCAGCATGTCAGTCT 309
 QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTPrThrPheGlyGly 100
 DB 310 GAAAGCTTGCAAGATTTCTGTCAGCAATATACATCTATCTCTCTCTCTCTCTCTCT 369
 QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
 DB 370 GGGACCAAGCTGAGCTTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
 QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
 DB 430 TCTGATGACAGATGTAATCTGGAATCTGCTTCTGTTGTGCTGCTGCTGCTGCTGCTGCT 489
 QY 141 ProArgGlnAlaLysValGlnTPrLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
 DB 490 CCAGAGAGGCCAAAGTACAGTGAAGGTGATACGCCCTCCAAATCGGGTAACTCCAG 549
 QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
 DB 550 GAGAGGTGTCAAGAGCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 609
 QY 181 LeuSerLysAlaAspTyrGlnLysValTyrAlaCysGlnValThrIleGlnGly 200
 DB 610 CTGAGCAAGCAGACATCAAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGGC 669

QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
Db 670 CTGAGCTGCCCGTCACAAAGAGCTTCAACAGGAGAGAGTGT 711

RESULT 5
LOCUS CO802834 714 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 24 from Patent EP1415998.
ACCESSION CO802834
VERSION CO802834.1 GI:47109852
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Heel,V., Koumenis,I., Leong,S.R., Presta,L.R., Shahrokh,Z. and Zapata,G.A.

TITLE Antibody fragment-polymer conjugates and humanized anti-IL-8
JOURNAL monoclonal antibodies
Genentech, Inc. (US)
Genentech, Inc. (US)
FEATURES
source 1..714
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 2,296-113 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.34 Conservative: 12
Best Local Similarity: 90.74 Mismatches: 8
Query Match: 91.14 Indels: 0
DB: 2 Gaps: 0
US-10-635-908-15 (1-214) x CO802834 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 70 GATATCGTCATGACACAGTCTCAAAATTCATGTCACATCAGTACAGAGACAGGCTCAGC 129

QY 21 IleThrCysLysAlaSerGlnAsnValAlaSerAlaValAlaTrpTyGlnGlnIlePro 40
Db 130 GTACACCTCGAAGCCAGATGAGATGGGTACTAATGATAGCTGATCAACAGAAACCA 189

QY 41 GlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
Db 190 GGGCAATCTCCCTAAAGCACTGATTTACTGTCATCTCCGCTACAGTGGAGTCCCTGAT 249

QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 250 CCTTCACAGGAGAGTGGATCTGGACAGATTTCATCTCACCATCAGCATGTGCACTGT 309

QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleTySerAsnTyProTrpThrPheGlyGly 100
Db 310 GAAGACTTGGCAGACATTTCTGTGACAGCAATATACATCTATCTCTCAGTTCGCTCT 369

QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGACCAAGCTCGAGCTTGAAGAGCTGTGGCTGCACCATCTGTCTTCTTCCCGCA 429

QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTy 140
Db 430 TCTGATGAGCACTTGAATCTGGAATCTGCTTGTGTGTGCTGCTGTAATACTTCTAT 489

QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyLysSerGln 160
Db 490 CCACAGAGAGCCAAAGTACAGTGAAGGTGAAGAACGCCCTCAATCGGGTAATCTCCAG 549

QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180

Db 550 GAGAGTGTACAGAGCAGACAGACAGACACTTACAGCTTCAGACACCCCTGACG 609

QY 181 LeuSerLysAlaAspTyrgLysHisLysValIleValIleValIleValIleValIle 200
Db 610 CTGAGCAAAAGCAGACTGACGAGAAACACAAAGCTTACGCTCGAAGTACCACTACAGG 669

QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
Db 670 CTGAGCTGCCCGTCACAAAGAGCTTCAACAGGAGAGAGTGT 711

RESULT 6
LOCUS AR233008 714 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 24 from patent US 6458355.
ACCESSION AR233008
VERSION AR233008.1 GI:27275392
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 714)
AUTHORS Heel,V., Koumenis,I., Leong,S., Presta,L., Shahrokh,Z. and Zapata,G.

TITLE Methode of treating inflammatory disease with anti-IL-8 antibody
JOURNAL fragment-polymer conjugates
Genentech, Inc.; South San Francisco, CA
Genentech, Inc. (US)
FEATURES
source 1..714
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2,296-113 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.34 Conservative: 12
Best Local Similarity: 90.74 Mismatches: 8
Query Match: 91.14 Indels: 0
DB: 2 Gaps: 0
US-10-635-908-15 (1-214) x AR233008 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 70 GATATCGTCATGACACAGTCTCAAAATTCATGTCACATCAGTACAGAGACAGGCTCAGC 129

QY 21 IleThrCysLysAlaSerGlnAsnValAlaSerAlaValAlaTrpTyGlnGlnIlePro 40
Db 130 GTACACCTCGAAGCCAGATGAGATGGGTACTAATGATAGCTGATCAACAGAAACCA 189

QY 41 GlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
Db 190 GGGCAATCTCCCTAAAGCACTGATTTACTGTCATCTCCGCTACAGTGGAGTCCCTGAT 249

QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 250 CCTTCACAGGAGAGTGGATCTGGACAGATTTCATCTCACCATCAGCATGTGCACTGT 309

QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleTySerAsnTyProTrpThrPheGlyGly 100
Db 310 GAAGACTTGGCAGACATTTCTGTGACAGCAATATACATCTATCTCTCAGTTCGCTCT 369

QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGACCAAGCTCGAGCTTGAAGAGCTGTGGCTGCACCATCTGTCTTCTTCCCGCA 429

QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTy 140
Db 430 TCTGATGAGCACTTGAATCTGGAATCTGCTTGTGTGTGCTGCTGTAATACTTCTAT 489

QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyLysSerGln 160

Db 490 CCCAGAGAGCCAAAGTACAGTGAAGGTGATACCCCTCCATCGGGTAACTCCAG 549
Qy 161 GUSerValThrgluGlnAspSerThySerLeuSerThrLeuThr 180
Db 550 GAGAGTGTACAGAGACGACGACGACGACGACGACGACGACGACGACGACGACG 609
Qy 181 LeuSerValAlaAspTyrGluTyrHisValTyrAlaCysGluValThrHisGlnGly 200
Db 610 CTGAGCAAGACAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCACTCAGAGGC 669
Qy 201 LeuSerSerProValThrThySerPheAsnArgGlyGlyCys 214
Db 670 CTGAGCTCGCCGCTCAACAAAGACTTCACAGGGGAGAGTGT 711

RESULT 7
LOCUS AR237939 714 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 24 from patent US 6468532.
ACCESSION AR237939
VERSION AR237939.1 GI:27282809
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 714)
Hseil,V., Koumenis,I., Leong,S., Presta,L., Shahrokh,Z. and Zapata,G.
TITLE Methods of treating inflammatory diseases with anti-IL-8 antibody
JOURNAL Fragment-polymer conjugates
Genentech, Inc.; South San Francisco, CA
Patent: US 6468532-A 24 22-OCT-2002;
Location/Qualifiers
FEATURES
source 1..714
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.29e-113 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AR237939 (1-714)

Qy 1 AspIleValMetThrglnSerGlnArgPheMetSerThrValGlyAspArgValSer 20
Db 70 GATATCGTCATGACACAGTCTCAAAATTCATGCCACATCAGTAGAGACAGGTCAGC 129
Qy 21 IleThrcysValAspSerGlnAsnValSerAlaValAlaTTPYrGlnGlnLysPro 40
Db 130 GTCACTGTCAAGGCGACGACGACGACGACGACGACGACGACGACGACGACGAC 189
Qy 41 GlnGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db 190 GGGCAATCTCTTAAGACGACGACGACGACGACGACGACGACGACGACGACGAC 249
Qy 61 ArgPheThrglySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 250 CGCTTCAACAGGACGATCTGGGACGATTTCACTCTCACATCAGCAGATGTCAGTCT 309
Qy 81 GlnAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTyrPheGlyGly 100
Db 310 GAAGACTTGGCAGACTATTTCTGTGCAATATTAACATCTATCTTCACGTTGGCTCT 369
Qy 101 GlnThryLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGCAAGCTGGAGCTTCAAGAGCTGTGGCTGCACCATCTGTCTTATCTTCCGCGCA 429
Qy 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140

Db 430 TCTGATGACAGTGTGAATCTGGAACCTGCTCTGTGTGTGCTGCTGAATACTTCTAT 489
Qy 141 ProArgGluAlaLysValGlnTTPYrValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 490 CCCAGAGAGCCAAAGTACAGTGAAGGTGATACCCCTCCAAATCGGGTAACTCCAG 549
Qy 161 GUSerValThrgluGlnAspSerThySerLeuSerThrLeuThr 180
Db 550 GAGAGTGTACAGAGACGACGACGACGACGACGACGACGACGACGACGACGACG 609
Qy 181 LeuSerValAlaAspTyrGluTyrHisValTyrAlaCysGluValThrHisGlnGly 200
Db 610 CTGAGCAAGACAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCACTCAGAGGC 669
Qy 201 LeuSerSerProValThrThySerPheAsnArgGlyGlyCys 214
Db 670 CTGAGCTCGCCGCTCAACAAAGACTTCACAGGGGAGAGTGT 711

RESULT 8
LOCUS 169460 714 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 27 from patent US 5677426.
ACCESSION 169460
VERSION 169460.1 GI:2831582
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 714)
Fong,S., Hebert,C., Alice., Kim,K., Jin. and Leong,S.R.
TITLE Anti-IL-8 antibody fragments
JOURNAL Patent: US 5677426-A 27 14-OCT-1997;
Location/Qualifiers
FEATURES
source 1..714
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.29e-113 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x 169460 (1-714)

Qy 1 AspIleValMetThrglnSerGlnArgPheMetSerThrValGlyAspArgValSer 20
Db 70 GATATCGTCATGACACAGTCTCAAAATTCATGCCACATCAGTAGAGACAGGTCAGC 129
Qy 21 IleThrcysValAspSerGlnAsnValSerAlaValAlaTTPYrGlnGlnLysPro 40
Db 130 GTCACTGTCAAGGCGACGACGACGACGACGACGACGACGACGACGACGACGAC 189
Qy 41 GlnGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db 190 GGGCAATCTCTTAAGACGACGACGACGACGACGACGACGACGACGACGACGAC 249
Qy 61 ArgPheThrglySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 250 CGCTTCAACAGGACGATCTGGGACGATTTCACTCTCACATCAGCAGATGTCAGTCT 309
Qy 81 GlnAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTyrPheGlyGly 100
Db 310 GAAGACTTGGCAGACTATTTCTGTGCAATATTAACATCTATCTTCACGTTGGCTCT 369
Qy 101 GlnThryLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGCAAGCTGGAGCTTCAAGAGCTGTGGCTGCACCATCTGTCTTATCTTCCGCGCA 429
Qy 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140


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Db      430  TCTGATGAGCAGTTGAAATCTGAACTGCTTCTGTGTGTCCTGCTGATTAATCTTAT 489
Qy      141  ProA:GGLUALALyValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAnsSerGln 160
Db      490  CCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATTAACGCCCTCCAAATCGGGTAATCCCGAG 549
Qy      161  GluSerValThrGluGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180
Db      550  GAGAGTGTCAAGAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 609
Qy      181  LeuSerLysAlaAspTrpGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200
Db      610  CTGAGCAAGACGACTACGAGAAACACAAAGCTTACGCTCGGAAATCACCCATCAGGAGC 669
Qy      201  LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
Db      670  CTGAGCTGCCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGT 711
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RESULT 9
LOCUS      I73079          714 bp      DNA      linear      PAT 03-APR-1998
DEFINITION Sequence 27 from patent US 5686070.
ACCESSION  I73079
VERSION     I73079.1  GI:3009218
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 714)
            Doerschuk,C.M., Fong,S., Hebert,C.Alice., Kim,K.Jin. and Leong,S.R.
            Methods for treating bacterial pneumonia
            Patent: US 5686070-A 27 11-NOV-1997;
            Location/Qualifiers
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                    source
                        1..714
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                        /mol_type="unassigned DNA"
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Alignment Scores:

Pred. No.:	2.29e-113	Length:	714
Score:	1017.00	Matches:	194
Percent Similarity:	96.3%	Conservative:	12
Best Local Similarity:	90.7%	Mismatches:	8
Query Match:	91.1%	Indels:	0
DB:	2	Gaps:	0

US-10-635-908-15 (1-214) x I73079 (1-714)

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Qy      1  AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db      70  GATATGTCATGACACAGTCTCAAAAATTCATGTCACATCAGTAGAGACAGGGTCAAG 129
Qy      21  IleThrCysLysValSerGlnAsnValValSerAlaValAlaTrpTyrglnGlnLysPro 40
Db      130  GTCACTTCGAAAGCCAGTCAAGATGTGGTACTTAAGTGAAGCTGGTATCAACGAAACCA 189
Qy      41  GlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
Db      190  GGGCAATCTCTTAAGACATGATTTACTGTCATCCGACCGTACAGTGAAGTCCCTGAT 249
Qy      61  ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db      250  CGCTTCACAGGCGAGTGAATCTGGACAGATTTCATCTCACATCCAGCCATGTGCAGTCT 309
Qy      81  GluAspLeuAlaAspPheCysGlnGlnTySerAsnTyProTrpThrPheGlyGly 100
Db      310  GAAGACTTGGCAACATATTTCTGTCAACATATTAACATCTATCTCTCACGTTCCGATCT 369
Qy      101  GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db      370  GGGACCAAGCTGGAGCTTGAAGAGGCTGTGGTGCACCAATCTGTCTTCACTTCCCGCCA 429
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Qy      121  SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTy 140
Db      430  TCTGATGAGCAGTTGAAATCTGAACTGCTTCTGTGTGTCCTGCTGATTAATCTTAT 489
Qy      141  ProA:GGLUALALyValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAnsSerGln 160
Db      490  CCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATTAACGCCCTCCAAATCGGGTAATCCCGAG 549
Qy      161  GluSerValThrGluGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180
Db      550  GAGAGTGTCAAGAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 609
Qy      181  LeuSerLysAlaAspTrpGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200
Db      610  CTGAGCAAGACGACTACGAGAAACACAAAGCTTACGCTCGGAAATCACCCATCAGGAGC 669
Qy      201  LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
Db      670  CTGAGCTGCCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGT 711
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RESULT 10
LOCUS      I79264          714 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 27 from patent US 5707622.
ACCESSION  I79264
VERSION     I79264.1  GI:3207554
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 714)
            Fong,S., Hebert,C.Alice., Kim,K.Jin. and Leong,S.R.
            Methods for treating ulcerative colitis
            Patent: US 5707622-A 27 13-JUN-1998;
            Location/Qualifiers
                FEATURES
                    source
                        1..714
                        /organism="Unknown"
                        /mol_type="unassigned DNA"
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Alignment Scores:

Pred. No.:	2.29e-113	Length:	714
Score:	1017.00	Matches:	194
Percent Similarity:	96.3%	Conservative:	12
Best Local Similarity:	90.7%	Mismatches:	8
Query Match:	91.1%	Indels:	0
DB:	2	Gaps:	0

US-10-635-908-15 (1-214) x I79264 (1-714)

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Qy      1  AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db      70  GATATGTCATGACACAGTCTCAAAAATTCATGTCACATCAGTAGAGACAGGGTCAAG 129
Qy      21  IleThrCysLysValSerGlnAsnValValSerAlaValAlaTrpTyrglnGlnLysPro 40
Db      130  GTCACTTCGAAAGCCAGTCAAGATGTGGTACTTAAGTGAAGCTGGTATCAACGAAACCA 189
Qy      41  GlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
Db      190  GGGCAATCTCTTAAGACATGATTTACTGTCATCCGACCGTACAGTGAAGTCCCTGAT 249
Qy      61  ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db      250  CGCTTCACAGGCGAGTGAATCTGGACAGATTTCATCTCACATCCAGCCATGTGCAGTCT 309
Qy      81  GluAspLeuAlaAspPheCysGlnGlnTySerAsnTyProTrpThrPheGlyGly 100
Db      310  GAAGACTTGGCAACATATTTCTGTCAACATATTAACATCTATCTCTCACGTTCCGATCT 369
Qy      101  GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db      370  GGGACCAAGCTGGAGCTTGAAGAGGCTGTGGTGCACCAATCTGTCTTCACTTCCCGCCA 429
```


QY 121 SerAspGluGlnIleuLysSerGlyThrAlaSerValCysLeuLeuAsnAspPheTyr 140
DB 430 TCGATGACAGAGTTGAATCTGAACTGCTTGTGTGTGCTGCTGAATTAATCTTAT 489
QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCAGAGAGGCCAAAGTACAGTGGAGGTGATGATGAGCCCTCCAAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGlnLysAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGTGTCAACAGAGCAGAGCAGACGACCTACAGCCTCAGCAGCAGCAGCAGCAGC 609
QY 181 LeuSerLysAlaAspTyrGluLysValTyrAlaCysGluValThrHisGlnGly 200
DB 610 CTAGCAAGACGACCTACGAGAAACAGAAAGTCTTACGCTGCGAAGTCAACCCATCAGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
DB 670 CTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 711

RESULT 11
187038 714 bp DNA linear PAT 10-JUN-1998
LOCUS Sequence 27 from patent US 5702946.
DEFINITION 187038
ACCESSION 187038.1 GI:3206756
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 714)
AUTHORS Doerschuk, C.M., Fong, S., Hebert, C.Alice, Kim, K.Jin, and Leong, S.R.
TITLE Anti-IL-8 monoclonal antibodies for treatment of inflammatory disorders
JOURNAL Patent: US 5702946-A 27 30-DEC-1997;
FEATURES
source location/Qualifiers
1..714
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.29e-113 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 0
DB: 2

US-10-635-908-15 (1-214) x 187038 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTACAGACAGCTCTCAAAATTTCAATGTCACATCATGAGAGAGAGGCTCAGC 129
QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 130 GTCACTGTCAAGGCCAGTCAAGATGTGGTACTAAATGATGCTGTATCAACAGAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAGCACTGATTTACTCGTCATCTTCACCGGTCAGGAGTCCCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGGACGAGTCTGGAGCAGATTTCACCTCACCATCAGCCATGTGCAAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
DB 310 GAAGCTTGACAGACTATTCTGTCAAGATTAATCACTATCTCTCAGCTTCGCTCT 369
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePhePro 120

DB 370 GGGACCAAGCTGAGAGCTTGAAGAGCTGTGGCTGACCAATCTGTCTTCACTCCGCCCA 429
QY 121 SerAspGluGlnIleuLysSerGlyThrAlaSerValCysLeuLeuAsnAspPheTyr 140
DB 430 TCGATGACAGAGTTGAATCTGAACTGCTTGTGTGTGCTGCTGAATTAATCTTAT 489
QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCAGAGAGGCCAAAGTACAGTGGAGGTGATGATGAGCCCTCCAAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGlnLysAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGTGTCAACAGAGCAGAGCAGACGACCTACAGCCTCAGCAGCAGCAGCAGCAGC 609
QY 181 LeuSerLysAlaAspTyrGluLysValTyrAlaCysGluValThrHisGlnGly 200
DB 610 CTAGCAAGACGACCTACGAGAAACAGAAAGTCTTACGCTGCGAAGTCAACCCATCAGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
DB 670 CTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 711

RESULT 12
AR647560 714 bp DNA linear PAT 20-APR-2005
LOCUS AR647560
DEFINITION Sequence 24 from patent US 6870033.
ACCESSION AR647560
VERSION AR647560.1 GI:62786643
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 714)
AUTHORS Heel, V., Koumentsis, I., Leong, S.R., Presta, L.G., Shahrokh, Z. and Zapata, G.A.
TITLE Antibody fragment-polymer conjugates and humanized anti-IL-8 monoclonal antibodies
JOURNAL Patent: US 6870033-A 24 22-MAR-2005;
Genentech, Inc.; South San Francisco, CA
FEATURES
source location/Qualifiers
1..714
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.29e-113 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 0
DB: 2

US-10-635-908-15 (1-214) x AR647560 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTACAGACAGCTCTCAAAATTTCAATGTCACATCATGAGAGAGAGGCTCAGC 129
QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 130 GTCACTGTCAAGGCCAGTCAAGATGTGGTACTAAATGATGCTGTATCAACAGAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAGCACTGATTTACTCGTCATCTTCACCGGTCAGGAGTCCCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGGACGAGTCTGGAGCAGATTTCACCTCACCATCAGCCATGTGCAAGTCT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100

|||||.....
Db 310 GAAAGCTTGACAGACTATTCTGTCGCAATATACATCTATCTCAGCTTCCT 369
Qy 101 G1YThrLysLeuGluIleLysArgThrValAlaIleProSerValPheIlePhePro 120
Db 370 GGGACCAAGCTGGAGCTTGGAGAGCTGGCTGCACCATCTGTTCTTCACTCCGCCA 429
Qy 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTyr 140
Db 430 TCTGAATGACAGAGTTGAATCTGGAACCTGCTTCGTGTGTGCTGCTGTAATACCTTCTAT 489
Qy 141 ProArgGluAlaLysValGlnTyrLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 490 CCCAGAGAGGCCAAAGTACAGTGGAGAGTGGATTAAGCCCTCCATCGGGTAACCTCCAG 549
Qy 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 550 GAGAGTGTCAAGAGAGAGACAGCAAGACAGCAGCCTCAGCAGCAGCAGCAGCAGCAG 609
Qy 181 LeuSerLysAlaAspTyrGluLysLysValTyrAlaCysGluValThrHisGlnGly 200
Db 610 CTGAGCAAAAGACACTACAGCAAGAAACAAAGTCTACGCTGCGAGAGTCAACCATCAGGC 669
Qy 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
Db 670 CTGAGCTCCGCCCTCACAAGAGCTTCAACAGGGAGAGTGT 711

RESULT 13
CS239095 1701 bp DNA linear PAT 04-JAN-2006
LOCUS Sequence 10 from Patent WO2005108989.
DEFINITION CS239095
ACCESSION CS239095
VERSION CS239095.1 GI:84365467
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 Chuntharapai, A.
AUTHORS Patent: WO 2005108989-A 10 17-NOV-2005;
JOURNAL GENENTECH, INC. (US)
FEATURES
source location/Qualifiers
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1684
/note="Unknown amino acid"

ORIGIN
unsure
/note="Unknown amino acid"

Alignment Scores:
Pred. No.: 1,06e-111 Length: 1701
Score: 1007.00 Matches: 193
Percent Similarity: 95.3% Conservative: 11
Best Local Similarity: 90.2% Mismatches: 10
Query Match: 90.2% Indels: 0
DB: Gaps: 0

US-10-635-908-15 (1-214) x CS239095 (1-1701)

Qy 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 109 GATATCGTATGACCCAGCTCTCAAGATTCTATGCCACATCAGTAGAGACAGGCTCAGC 168
Qy 21 IleThrCysAlaLysSerGlnAsnValIleSerAlaValIleTyrGlnGlnLysPro 40
Db 169 GTCACTCGCAAGGCGCACTGACAGCTGGATATCACTATAGCTGGATCAACGAAACTA 228
Qy 41 GlyGlnSerProLysLeuLeuIleLysSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db 229 GGGCAATCTCTAAACACATGATTACTCGGCATCTTACCGGTGTAGTGGGTCCCTGAT 288

Qy 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 289 CCGTTCACAGGAGGAGATCTCGACAGATTTCACCTCACCATACCAATGTCAGTCT 348
Qy 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrPheGlyGly 100
Db 349 GAAAGCTTGCGAGAGTATTCTGTGACGAAATTCACAGTTTCCGTCGACGTTCCGTGA 408
Qy 101 G1YThrLysLeuGluIleLysArgThrValAlaIleProSerValPheIlePhePro 120
Db 409 GGTACCAAGGTGAGATCAACGAACTGGCTGCACCATCTGTTCTTCACTTCCGCCCA 468
Qy 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTyr 140
Db 469 TCTGAATGACAGAGTTGAATCTGGAACCTGCTTCGTGTGTGCTGCTGTAATACCTTCTAT 528
Qy 141 ProArgGluAlaLysValGlnTyrLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 529 CCCAGAGAGGCCAAAGTACAGTGGAGAGTGGATTAAGCCCTCCATCGGGTAACCTCCAG 588
Qy 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 589 GAGAGTGTCAAGAGAGAGACAGCAAGACACACCTCAGCAGCAGCAGCAGCAGCAG 648
Qy 181 LeuSerLysAlaAspTyrGluLysLysValTyrAlaCysGluValThrHisGlnGly 200
Db 649 CTGAGCAAAAGACACTACAGCAAGAAACAAAGTCTACGCTGCGAGAGTCAACCATCAGGC 708
Qy 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
Db 709 CTGAGCTCCGCCCTCACAAGAGCTTCAACAGGGAGAGTGT 750

RESULT 14
CS133169 699 bp DNA linear PAT 02-AUG-2005
LOCUS Sequence 14 from Patent WO2005063299.
DEFINITION CS133169
ACCESSION CS133169
VERSION CS133169.1 GI:71792256
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 Chang, W.
AUTHORS Compositions and methods for the treatment of tumor of
TITLE hematopoietic origin
JOURNAL Patent: WO 2005063299-A 14 14-JUL-2005;
Genentech, Inc. (US)
FEATURES
source location/Qualifiers
1..699
/organism="Homo sapiens"
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ORIGIN
unsure
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Alignment Scores:
Pred. No.: 1.4e-108 Length: 699
Score: 977.50 Matches: 190
Percent Similarity: 94.4% Conservative: 12
Best Local Similarity: 88.8% Mismatches: 11
Query Match: 87.6% Indels: 1
DB: Gaps: 1

US-10-635-908-15 (1-214) x CS133169 (1-699)

Qy 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 58 GATATCGTATGACCCAGCTCTCAAGATTCTATGCCACATCAGTAGAGACAGGCTCAGC 117
Qy 21 IleThrCysAlaLysSerGlnAsnValIleSerAlaValIleTyrGlnGlnLysPro 40

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          /db_xref="GI:57337319"
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gene      928. .1635
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CDS       928. .1635
          /gene="IGK"
          /note="mouse-human chimera"
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          /protein_id="CAH65831.1"
          /db_xref="GI:57337320"
          /translation="MKOSTIALALLPLFTPTPKADIELQSPSSLASVDKRYTITC
          KASQGVNVAWYQOKPKAPKVLIVSASVYSGVPFSGSGSGTPTLTISLQEE
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          /note="hOa signal peptide"
          991. .1632
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          /product="light chain"
          1647. .1721
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          1723. .2168
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gene      2310. .3170
          /gene="bia"
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          /protein_id="CAH65832.1"
          /db_xref="GI:57337321"
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gene      3180. .3803
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CDS       3180. .3803
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Db		433	TCTGATGAGCACTTGAAAATTCTGGAACTGCCCTGTGTGTGGCTGCTGAATTAATCTTAT	492
Oy		141	ProArgIuaIAlaLysValGIntPrLyVaIAspAsnaIAlenuInSerGIyaensergIn	160
Db		493	CCCAGAAGAGGCCCAAAGTACAGTGGAAAGTGGATTAACGCCCTCCAAATCGGGTAATCCAC	552
Oy		161	GluservalThrGIUGlnAsperLyAspSerThrtTySerieseuserSerThreuthr	180
Db		553	GAGAGTGTCAACAGAGCAGGACAGCAAGAACAGACCACTTACAGCCTCAGCACACCCTGACG	612
Oy		181	LeuSerLyVaIAspTYrGIuLyShILysValITyrAlaCYsgGIuValThrhISgInGLY	200
Db		613	CTGAGCAAGACGAGACTACAGAAACACAAAGTTACGCTTCGCAAGTCAACCCATCAGAGC	672
Oy		201	LeuSerSerProValThrLySerPheasnArgIyGIuCyS	214
Db		673	CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGAGT	714
RESULT 4				
AAT62933	ID	AAT62933	standard; DNA; 5250 BP.	
XX	AC	AAT62933;		
XX	DT	17-OCT-2003	(revised)	
DT	DT	16-JUN-1997	(first entry)	
XX	DE	2A2 human IgG4 expression plasmid insert sequence.		
XX	KM	Xenotransplantation; graft rejection; cell interaction; pig;		
KM	KW	vascular cell adhesion molecule; VCAM; monoclonal antibody;		
KW	XX	chimeric antibody; diagnosis; ss.		
OS	OS	Homo; sapiens.		
OS	OS	Mus sp.		
XX	XX	Chimeric.		
FT	FH	Key	Location/Qualifiers	
FT	FT	exon	/tag= a 903..1055	
FT	FT	intron	/tag= b 1056..1285	
FT	FT	exon	/tag= c 1286..2020	
FT	FT	intron	/codon_start= 1318 2021..2410	
FT	FT	exon	/tag= d 2411..2446	
FT	FT	intron	/tag= e 2447..2564	
FT	FT	exon	/tag= f 2565..2894	
FT	FT	intron	/tag= g 2895..2991	
FT	FT	exon	/tag= h 2992..3314	
FT	FT	intron	/tag= i 3315..4045	
FT	FT	exon	/tag= j 4046..4198	
FT	FT	intron	/tag= k 4199..4428	
FT	FT	exon	/tag= l 4429..5177	
FT	FT	intron	/codon_start= 4461	
XX	FN	WO9711971-A1.		
XX	XX			

```

PD 03-APR-1997.
PF 27-SEP-1996; 96MO-US015575.
XX
XX 28-SEP-1995; 95US-0004489P.
PR 26-SEP-1996; 96US-00004489.
XX
XX (ALEX-) ALEXION PHARM INC.
PA
PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matie LA;
DR WPI; 1997-212855/19.
XX
XX P-PSDB; AAM14935, AAM14936.
PT
PT Antibodies binding to porcine but not human cell interaction proteins -
PT useful to treat and assay for rejection of xenografted porcine organs,
PT tissues or cells.
PS
PS Disclosure; Page 47-52; 105pp; English.
XX
XX A DNA sequence (AA762933) comprises a 2A2 human IgG4 expression plasmid
XX insert sequence. It is obd. by cloning the ligh chain (see also
XX AA762929) and heavy chain (see also AA762930) variable region sequences
XX of murine anti-porcine vascular cell adhesion molecule (VCAM) monoclonal
XX antibody 2A2 into an expression plasmid modified to contain the human
XX gamma4 constant region in plasmid of the human gamma C1 region. The
XX encoded heavy chain (AAM14935) and light chain (AAM14936) can be used to
XX produce a chimeric antibody that is specific for porcine VCAM. The
XX chimeric antibody is useful for diagnosing human rejection of porcine
XX xenotransplants and for improving xenotransplantation of porcine cells,
XX tissues and organs into human recipients. (Updated on 17-OCT-2003 to
XX standardise OS field)
SQ Sequence 5250 BP; 1236 A; 1469 C; 1352 G; 1193 T; 0 U; 0 Other;

Alignment Scores:
Pred. NO.: 6.27e-81 Length: 5250
Score: 1021.00 Matches: 194
Percent Similarity: 96.7% Conservative: 13
Best Local Similarity: 90.7% Mismatches: 7
Query Match: 91.5% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AAT62933 (1-5250)
QY 1 AsptIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 4533 GACATTTGGAAGACCACCGCTCCAAAATTCAATGTCACATATTAAGAGACAGGCTCAGC 4592
QY 21 IleThrCysIleValAspGlnAsnValValSerAlaValAlaTPTyrGlnGlnIlePro 40
DB 4593 GTCACTCGCAAGCGCAGTCAGAAATGTGGGTCTTAATGATGCTGTTCACACAGAAACCA 4652
QY 41 GlyIleSerProIleLeuLeuIleTyrSerAlaSerAsnAlaGlyTyrThrGlyValProAsp 60
DB 4653 GGCCACGCTCTCTAAACACATTAATTACTCGGCATCTTCGCCCTACAGGAGTCCCGAT 4712
QY 61 ArgPheThrGlySerGlySerGlyTyrThrAspPheThrLeuThrIleSerAspMetGlnSer 80
DB 4713 CGCTTCACAGGACAGGAGTCTGGACACGATTTCACTTCACACATCCAAATGTGCACTCT 4772
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleTyrSerAsnTyrProTyrThrPheGlyGly 100
DB 4773 GAAGACTTGGCAGAGATTTCTGTGCATCAATATAATCCCTATCTCTCAGCTTCGGGGGG 4832
QY 101 GlyThrIleLeuGluIleIleValArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 4833 GGGACCAAGCTGGAATAATAAACGAACGTGTGCTCAGCACCATTGTCTTCATCTTCCGCCA 4892
QY 121 SerAspGluGlnIleLeuIleValSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTyr 140
DB 4893 TCTGATGCGCACTTGAAATCTTGAACTGCTCTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 4952

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[illegible]

Qy	161	GLuSerVal1ThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr	180		
Db	550	GAGAGTGTCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG	609		
Qy	181	LeuSerLysAlaAspTyrGluGlyHisLysValTyrIaCYsGluValThrHisGlnGly	200		
Db	610	CTGAGCAAGACAGACTACGAGAAACACAAAGTCAGCTCGGAAAGTCAACCATCAGGC	669		
Qy	201	LeuSerSerProVal1ThrLysSerPheAsnArgGlyGluCys	214		
Db	670	CTGAGCTCGCCCGTCAACAAAGAGCTTCAACAGGGAGAGAGTGT	711		
RESULT 8					
ID	AAV03206	standard; DNA, 714 BP.			
XX	AAV03206;				
XX	17-OCT-2003	(revised)			
DT	15-APR-1998	(first entry)			
XX	Murine variable and human IgG1 constant region light chain DNA.				
XX					
KM	Light chain; heavy chain; monoclonal antibody; interleukin-8; IL-8;				
KM	inflammatory disorder; bacterial pneumonia; neutrophil chemotaxis;				
KM	anti-IL-8 monoclonal antibody; IL-8 mediated elastase release;				
KM	Streptococcus pneumoniae; Escherichia coli; Pseudomonas aeruginosa;				
XX	ulcerative colitis; ds.				
XX					
OS	Mus sp.				
OS	Homo sapiens.				
XX	Chimeric.				
XX					
FX	Key	Location/Qualifiers			
FT	CDS	1..714			
FT		/*tag= a			
FT	misc_feature	1..395			
FT		/*tag= c			
FT		/note= "encodes the variable light chain region of the			
FT		murine antibody 5.12.14"			
FT	sig_peptide	1..69			
FT		/*tag= b			
FT	misc_feature	396..714			
FT		/*tag= d			
FT		/note= "encodes the constant light chain region of human			
FT		IgG1"			
XX					
PN	US5686070-A.				
XX					
PD	11-NOV-1997.				
XX					
PF	01-MAR-1995;	95US-00398612.			
PR	03-MAR-1994;	94US-00205864.			
XX					
PA	(INDV) UNIV INDIANA.				
XX	(GETH) GENENTECH INC.				
XX					
PI	Kim KJ, Doerschuk CM, Leong SR, Fong S, Hebert CA;				
XX					
DR	WPI; 1997-558085/51.				
XX	P-PSDB; AAW42319.				
PT	Treatment of bacterial pneumonia - with monoclonal antibody specific for				
XX	interleukin-8; inhibits lung inflammatory conditions.				
XX					
PS	Disclosure; Fig 19; 63pp; English.				
XX					
CC	The present sequence depicts the coding sequence for murine monoclonal				
CC	antibody 5.12.14 light chain variable region and the human IgG1 light				
CC	chain constant region. The 5.12.14 antibody is a murine anti interleukin				
CC	8 (IL-8) IgG2a isotype. IL-8 is a neutrophil chemotactic peptide secreted				


```

QY 1 AsplleValMeThrgInserGlnArgPheMeSerThrThrValGlyAspArgValSer 20
Db 70 GATATGCTCATGACACAGTCTCAAAAATTCATCTCCACATCATAGAGACAGGGTCCAG 129
QY 21 IleThrCysAlaSerGlnAsnValValSerAlaValAlaTPrYrGlnGlnIlePro 40
Db 130 GTCACTGCAAGGCCAGTCAAGATGTGGGACTAATGTAGCCCTGTATCAACAGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleYrSerAlaSerAsnArgYrThrGlyValProAsp 60
Db 190 GGGCAATCTCTTAAACACATGATTTACTCTCTACCGTACAGTGGAGTCCCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIleSerAsnMetGlnSer 80
Db 250 CGCTTACAGGAGCTGATGATGGACAGATTTCACTCTCCATCCATGACCATGTGCGATCT 349
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnYrSerAsnYrProTPrThrPheGlyGly 100
Db 310 GAAGACTGGCAGACTATTTCTGTACAGCATATATACATCTATCTCTCAGGTCGGTCCCT 369
QY 101 GlyThrIleLeuGlnIleYrArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGACCAAGCTGAGCTTCAAGAGCTGTGCTGACCATCTGTCTCATCTTCCGCCCA 429
QY 121 SerAspGlnGlnIleuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db 430 TCTGATGACGAGTTGAAATCTGGAACCTCTTCTTCTGTGCTGCTGGAATTAATCTTAT 489
QY 141 ProArgGlnAlaIleYrValGlnTPrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 490 CCCAGAGAGGCCAAAGTACAGTGAAGTGAATACCCCTCCCATAGGGTAACTCCACAG 549
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrYrSerLeuSerSerThrLeuThr 180
Db 550 GAGAGTGTCAAGAGCAGACAGACAGACAGACAGCCCTACAGCCCTCAGCAGACCTTACG 609
QY 181 LeuSerIleValAlaAspYrGlnIleYrHisIleValTyrAlaCysGlnValIleThrHisGlnGly 200
Db 610 CTGAGCAAGCAGACTCTCGAGAAACACAAAGCTTACCCCTCGCAAGTCAACCATCAGAGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys 214
Db 670 CTGAGCTCGCCCGTCAACAAAGAGCTTCAACAGGGGAGAGTCT 711
RESULT 10
ID AAV55098 standard; cDNA; 714 BP.
AC AAV55098;
XX
DT 17-OCT-2003 (revised)
DT 15-FEB-1999 (first entry)
XX
DE Anti-IL-8 mouse-human chimeric Fab 5.12.14 light chain DNA.
XX
KW Humanised antibody; chimeric antibody; monoclonal antibody; mouse; human;
KW Fab; interleukin-8; inflammation; immunotherapy; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW ischaemic reperfusion; adult respiratory distress syndrome; dermatitis;
KW meningitis; encephalitis; uveitis; autoimmune disease;
KW rheumatoid arthritis; Sjogren's syndrome; vasculitis;
KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis; vasculitis;
KW bronchitis; bronchiectasis; cystic fibrosis; diagnosis; therapy; de.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT 1..714
FT CDS /*tag= a

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```

FT sig_peptide 1..69
FT /*tag= b
FT /note= "STII signal peptide"
FT mat_peptide 70..711
FT /*tag= c
FT /product= "mouse-human chimeric light chain"
XX
XX MO9837200-A2.
XX
XX 27-AUG-1998.
XX
XX 20-FEB-1998; 98WO-US003337.
XX
XX 21-FEB-1997; 97US-00804444.
XX
XX 22-JAN-1998; 98US-00012116.
XX
XX (GENTH ) GEMENTECH INC.
XX
XX Hsei V, Kouments I, Leong SR, Presta LR, Shahrokh Z, Zapata GA;
XX
XX MPI; 1998-467563/40.
XX
XX P-PSDB; AAW69307.
XX
XX New conjugates of antibody fragments - having covalently attached non-
XX proteinaceous polymer molecules, particularly polyethylene glycol, for
XX improving the residence time in the circulation.
XX
XX Example D; Fig 19; 328pp; English.
XX
XX This DNA sequence encodes a polypeptide (see AAW69307) comprising the
XX light chain variable region of murine anti-interleukin-8 (IL-8)
XX monoclonal antibody (MAb) 5.12.14 (see AAW69305) and the human IgG1 light
XX chain constant region. It was obtained by PCR amplification (see AAV55094
XX -95) and has been utilised in the construction of 5.12.14 Fab vector
XX pentiIL-8-2 (ATCC 97056). Humanised anti-IL-8 MAbs are described for use
XX in diagnostic applications and in the treatment of inflammatory
XX disorders. The invention provides conjugates of an antibody fragment and
XX a polymer, such as PEG, that have improved half-life, mean residence
XX time, and/or clearance rate. The conjugates can be used for immune
XX therapy of e.g. psoriasis, responses associated with inflammatory bowel
XX disease (such as Crohn's disease and ulcerative colitis), ischaemic
XX reperfusion, adult respiratory distress syndrome, dermatitis, meningitis,
XX encephalitis, uveitis, autoimmune diseases such as rheumatoid diapedesis,
XX Sjogren's syndrome, vasculitis, diseases involving leukocyte diapedesis,
XX central nervous system inflammatory disorder, multiple organ injury
XX CC syndrome secondary to septicemia or trauma, alcoholic hepatitis,
XX CC bacterial pneumonia, antigen-antibody complex mediated diseases,
XX CC inflammations of the lung, including pleurisy, alveolitis, vasculitis,
XX CC pneumonia, chronic bronchitis, bronchiectasis, and cystic fibrosis.
XX (Updated on 17-OCT-2003 to standardise OS field)
XX
XX
SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;
XX
XX
Alignment Scores:
Pred. No.: 1.55e-81 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 2 Gaps: 0
XX
US-10-635-908-15 (1-214) x AAV55098 (1-714)
QY 1 AsplleValMeThrgInserGlnArgPheMeSerThrThrValGlyAspArgValSer 20
Db 70 GATATGCTCATGACACAGTCTCAAAAATTCATCTCCACATCATAGAGACAGGGTCCAG 129
QY 21 IleThrCysAlaSerGlnAsnValValSerAlaValAlaTPrYrGlnGlnIlePro 40
Db 130 GTCACTGCAAGGCCAGTCAAGATGTGGGACTAATGTAGCCCTGTATCAACAGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleYrSerAlaSerAsnArgYrThrGlyValProAsp 60

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Db 190 GGGCAATCTCTTAAGACTGATTTACTGTCTACCTACCGGTACAGTGGATCCCTGAT 249
Qy 61 ArgpHeThrGlySerGlySerGlyThraaPheThrLeuThrIleSerAnMeGInser 80
Db 250 CCCTTCACAGGAGGTGATCTGGACAGATTCTCACTCACCATCAGCATGTGACAGTCT 309
Qy 81 GluaaPLeuAlaAaPhePheCysGInGInTyrsSerAaNTyrProTrpThrPheGlyGly 100
Db 310 GAAGACTTGACAGACTATTCTGTCTGACCAATATACATCTATCTCTCACTCCGTTCCGTTCT 369
Qy 101 GlyThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGACCAACTGGAGCTTGGAGAGCTGTGGCTGCACCATCTGTCTTCACTTCCCGCA 429
Qy 121 SerAaPGLuGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAnAaPheTyr 140
Db 430 TCTGATGACAGCAAGTTGAATCTGCAACTGCTTCTGTGTGTGCTGCTGCAATAACTTCTAT 489
Qy 141 ProArgGluAlaLysValGlnTrpLysValAaPaaAnaIleuGlnSerGlyLysAnserGln 160
Db 490 CCCAGAGAGGCCAAAGTACAGTGAAGAGTGAATTAAGCCCTCCAAATCGGGTAACTCCAG 549
Qy 161 GluSerValThrGluGlnAaPseLysAaPseThrTyrSerLeuSerSerThrLeuThr 180
Db 550 GAGAGTGTACAGAGCAGACAGACCAAGACAGACCTTACAGCAGCAGCAGCAGCAG 609
Qy 181 LeuSerLysAlaAaPTrpGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200
Db 610 CTGAGCAAAAGCAGACTACGAGAAACAAAGTCTACGCTGCGCAAGTCAACCATCAGGGC 669
Qy 201 LeuSerSerProValThrLysSerPheAnaArgLysGluCys 214
Db 670 CTGAGCTCGCCGTCAAAAGACTTCAACAGGGGAGAGTGT 711
```

RESULT 11

AAV10292
AAV10292 standard; DNA; 714 BP.

AAV10292;

03-JUN-1998 (first entry)

Mab 5.12.14 and human IgG1 construct light chain region DNA.

Monoclonal antibody; Mab 5.12.14; interleukin-8; IL-8; anti-IL-8; murine;
ulcerative colitis; immunotherapy; bacterial pneumonia; variable region;
treatment; light chain; heavy chain; neutrophil chemotaxis inhibitor;
human; IgG1; constant region; ss.

Synthetic.

Key Location/Qualifiers

CDS 1..714

FT 1..69

FT 70..714

FT 70..714

FT 70..714

FT 70..714

FT 70..714

FT 70..714

FT 70..714

FT 70..714

FT 70..714

/product= "5.12.14-IgG1 construct"
/note= "5.12.14 light chain variable region and human
IgG1 light chain constant region construct"

```
XX MPI; 1998-100296/09.
DR P-PSDB; AAV40122.
XX Immunotherapy of ulcerative colitis - with monoclonal antibody specific
PT for interleukin-8.
XX Example B; Fig 19; 63pp; English.
XX This sequence encodes the murine 5.12.14 (anti-IL-8) monoclonal antibody
CC (Mab) light chain variable region and the human IgG1 light chain constant
CC region construct. This construct is used in a novel method for treating
CC ulcerative colitis which involves the administration of an anti-IL-8
CC monoclonal antibody capable of binding to human interleukin-8 (IL-8) with
CC a Kd of 10-8 to 10-11 M. This Mab also inhibits neutrophil chemotaxis in
CC response to IL-8, inhibits IL-8-mediated elastase release by neutrophils
CC and does not bind to C5a, beta -TG or platelet factor 4. The anti-IL-8
CC antibodies can also be used for the treatment of bacterial pneumonia
XX
SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.55e-81 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x AAV10292 (1-714)

Qy 1 AaPIIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAaPArgValSer 20
Db 70 GATATCGTATACACAGTCTCAAAATTCATGTCATCATCATGAGAGAGAGGATCAGC 129
Qy 21 IleThrCysLysAlaSerGlnAaAnaValIleSerAlaValAlaIleTrpGlnGlnLysPro 40
Db 130 GTCACCTGCAAGCCAGCTAGATGTGGGTACTAATGTAGCTCGGTATCAACAGAAACCA 189
Qy 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAaNTyrThrGlyValProAaP 60
Db 190 GGGCAATCTCTTAAGACTGATTTACTGTCTACGCAATATACATCTATCTCAGTCCGTTCT 249
Qy 61 ArgpHeThrGlySerGlySerGlyThraaPheThrLeuThrIleSerAnMeGInser 80
Db 250 CCCTTCACAGGAGGTGATCTGGACAGATTCTCACTCACCATCAGCATGTGACAGTCT 309
Qy 81 GluaaPLeuAlaAaPhePheCysGInGInTyrsSerAaNTyrProTrpThrPheGlyGly 100
Db 310 GAAGACTTGACAGACTATTCTGTCTGACCAATATACATCTATCTCTCACTCCGTTCT 369
Qy 101 GlyThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGACCAACTGGAGCTTGGAGAGCTGTGGCTGCACCATCTGTCTTCACTTCCCGCA 429
Qy 121 SerAaPGLuGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAnAaPheTyr 140
Db 430 TCTGATGACAGCAAGTTGAATCTGCAACTGCTTCTGTGTGTGCTGCTGCAATAACTTCTAT 489
Qy 141 ProArgGluAlaLysValGlnTrpLysValAaPaaAnaIleuGlnSerGlyLysAnserGln 160
Db 490 CCCAGAGAGGCCAAAGTACAGTGAAGAGTGAATTAAGCCCTCCAAATCGGGTAACTCCAG 549
Qy 161 GluSerValThrGluGlnAaPseLysAaPseThrTyrSerLeuSerSerThrLeuThr 180
Db 550 GAGAGTGTACAGAGCAGACAGACCAAGACAGACCTTACAGCAGCAGCAGCAGCAG 609
Qy 181 LeuSerLysAlaAaPTrpGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200
Db 610 CTGAGCAAAAGCAGACTACGAGAAACAAAGTCTACGCTGCGCAAGTCAACCATCAGGGC 669
Qy 201 LeuSerSerProValThrLysSerPheAnaArgLysGluCys 214
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Db 670 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGAGAGTGT 711

RESULT 12
AAK90576
ID AAK90576 standard; DNA; 714 BP.
XX
XX AAK90576;
AC
XX
DT 05-OCT-1999 (first entry)
XX
XX 5.12.14 L chain V region and human IgG1 L chain constant region DNA.
DE
XX
XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
KM diagnosis; inflammatory disorder; conjugate; immunoglobulin;
KM fusion protein; ss.
XX
XX Synthetic.
OS Mus musculus.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..714
FT /*tag= a
XX
XX MO9937779-AI.
XX
XX 29-JUL-1999.
XX
XX 19-JAN-1999; 99MO-US001081.
XX
XX 22-JAN-1998; 98US-00012116.
PR 20-FEB-1998; 98MO-US003337.
PR 24-JUL-1998; 98US-00121952.
PR 24-JUL-1998; 98US-00122513.
XX
XX (GETH) GENENTECH INC.
XX
XX Heel V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z, Zapata GA;
XX WPI; 1999-469134/39.
DR P-PSDB; AAY29446.
XX
XX New conjugates of nonproteinaceous polymers with antibody fragments, used
PT for treating inflammatory disorders.
XX
PS Disclosure; Fig 19; 360pp; English.
XX
XX The present invention describes a novel conjugate having one or more
CC antibody fragments covalently attached to one or more nonproteinaceous
CC polymer molecules, where the apparent size of the conjugate is at least
CC about 500 kDa. Conjugates of antibody fragments which bind the human
CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC treating inflammatory disorders e.g. acute lung injury, ischaemic
CC reperfusion disorder, and autoimmune diseases. They can also be used for
CC treating e.g. inflammatory skin diseases including psoriasis and atopic
CC dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases.
CC The conjugates can also be used as reagents in an animal model system for
CC in vivo study of the biological functions of the antigen recognised by
CC the conjugate. The present sequence encodes the 5.12.14 light chain
CC variable region and the human IgG1 light chain constant region fusion
CC protein from the present invention
XX
SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.55e-81 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 2 Gaps: 0
US-10-635-908-15 (1-214) x AAK90576 (1-714)

QY 1 AspllevalmetTh-GlnSerGlnArGhetSerThrValGlyAspArgValSer 20
Db 70 GATATGTCATGACACAGCTCAAAAATTCATGTCACATGAGAGACGGGTCAAC 129
QY 21 IleThrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnLysPro 40
Db 130 GTACCTGCAGGCCAGTCAGATGGGTACTAATGTCGCTGGTATCAACGAAACCA 189
QY 41 GylGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrGlyValProAsp 60
Db 190 GGGCAATCTCCAAAGCACTGATTTACTGTCATCTACCGGTACAGTGGACCTCGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 250 CGCTTCACAGCAGTGGATCTGGACAGATTCACCTCACATCCATCGCATGTGCAGTCT 309
QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProThrThrPheGlyGly 100
Db 310 GAAGACTTGACAGACTATTCTGTCAAGATTAATACATCTATCTCACGTTCCGGTCT 369
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePhePro 120
Db 370 GGGACCAAGCTGAGAGCTTGAAGAGCTGGTGCACCACTGTCTTCACTTCCGCCCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db 430 TCTGATGACAGATTGAATCTGGAATCTGCTTGTGTGTGCTGTGATTAATCTTCTAT 489
QY 141 ProArgGlnAlaLysValGlnTyrPlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 490 CCAGAGAGGCCAAAGTACGTGAAGGTGATPAAGCCCTCCAAATCGGGTAATCTCCAG 549
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 550 GAGAGTGTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 609
QY 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGlnValThrIleGlnGly 200
Db 610 CTGAGCAAGCAGACGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCAACCACTCAGG 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
Db 670 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGAGAGTGT 711

RESULT 13
AAZ87952
ID AAZ87952 standard; DNA; 714 BP.
XX
AC AAZ87952;
XX
DT 15-SEP-2003 (revised)
DT 06-JUN-2000 (first entry)
XX
XX Chimeric anti-IL-8 antibody light chain DNA sequence.
DE
XX Interleukin-8; IL-8; monoclonal antibody; Mab; anti-IL-8; 6G4.2.5Y1N35A;
KM inflammatory disorder; adult respiratory distress syndrome; mouse;
KM affinity purification; 5.12.14; ds.
XX
XX Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
XX US6025158-A.
XX
XX 15-FEB-2000.
PD
XX 20-FEB-1998; 98US-00027449.
PF
XX 21-FEB-1997; 97US-0038664P.
PR 22-JAN-1998; 98US-0074330P.
XX

PA (GETH) GENENTECH INC.
 XX Presta LG, Leong SR, Gonzalez TN;
 XX WPI; 2000-181809/16.
 DR P-PSDB; AAY77744.
 XX
 PT New nucleic acid molecule encodes a polypeptide which is an anti-
 PT interleukin-8 monoclonal antibody or antibody fragment useful for the
 PT production of anti-interleukin-8 monoclonal antibodies or fragments.
 XX
 PS Example; Fig 19; 188bp; English.
 XX
 CC The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
 CC (Mab). The anti-IL-8 Mab comprises a sequence containing the CDRs
 CC (complementarity determining regions) of the humanized anti-IL-8
 CC 6G4.2.5V11N35A light chain; and amino acids 24-253 of the humanized anti-
 CC IL-8 6G4.2.5V11N35A heavy chain. The anti-IL-8 Mabs and fragments can be
 CC used in diagnosis, for affinity purification of IL-8 from recombinant
 CC cell culture or natural sources and for the treatment of inflammatory
 CC disorders e.g. adult respiratory distress syndrome. Nucleic acids
 CC encoding the anti-IL-8 Mab can be associated in a vector with another
 CC gene encoding another protein or protein fragment to produce a fusion
 CC protein which can make isolation and/or purification of the protein an
 CC easier process. The present sequence represents the nucleotide sequence
 CC of murine anti-IL-8 antibody 5.12.14 light chain variable region and the
 CC human IgG1 light chain constant region. (Updated on 15-SEP-2003 to
 CC standardise OS field)
 CC
 SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 1,55e-81 Length: 714
 Score: 1017.00 Matches: 194
 Percent Similarity: 96.3% Conservative: 12
 Best Local Similarity: 90.7% Mismatches: 8
 Query Match: 91.1% Indels: 0
 DB: 3 Gaps: 0
 US-10-635-908-15 (1-214) x AA287952 (1-714)
 QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
 DB 70 GATATGTCATGACACAGTCTCAAAATTCATCTCCACATAGAGACAGCGGTACG 129
 QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTPrpYngInlyPro 40
 DB 130 GTCACTCGCAAGCCGATCGAATGTGGTACTAATGTAGCCCTGATCAACGAAACCA 189
 QY 41 GlyGlnSerProLysLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
 DB 190 GGGCAATCTCTTAAGCACATGATTACTCTCATCTACCGAGTGGAGTGGTCCCTGAT 249
 QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
 DB 250 CGCTTCACAGGAGCGATGATCTGGACACAGATTTCATCTCAACATGACATGTCAGTCT 309
 QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTPrpThrPheGlyGly 100
 DB 310 GAAGACTTGGCAACATATTCTGTCTGACGATATATACATCATCTCTCAAGTTCGGTCT 369
 QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
 DB 370 GGGACCAAGCTGAGCTTCAAGAGCTGTGGCTGACACATCTCTTTCATCTCCGCCCA 429
 QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
 DB 430 TCTGATGAGACAGTTGAATCTGGAACCTGTTCTGTGTGGTGGCTGGAATACTCTTAT 489
 QY 141 ProArgGlnAlaLysValGlnTPrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
 DB 490 CCCAGAGAGGCCCAAGATACAGTGGAGGTGATTAACGCCCTCCCAATCGGGTAACTCCAG 549

QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
 DB 550 GAGAGTGTCAACAGACAGACAGACAGACAGACATCTACGCTACAGACACCTTGACG 609
 QY 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200
 DB 610 CTGACCAAGACGACGACTACAGAGAACACAAAGCTACGCTCGGAGATGCCATCAGGCG 669
 QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
 DB 670 CTGAGCTCGCCCGTCAAAAGAGCTTCAACAGCGGAGAGGTGT 711
 RESULT 14
 AAC65491
 ID AAC65491 standard; DNA; 714 BP.
 XX
 AC AAC65491;
 XX
 DT 12-FEB-2001 (first entry)
 XX
 DE 5-12-14 antibody light chain V region coding sequence SEQ ID NO: 24.
 XX
 KW Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
 KW adult respiratory distress syndrome; multiple organ failure;
 KW bacterial pneumonia; inflammatory bowel disease; de.
 XX
 OS Unidentified.
 XX
 PN US6133426-A.
 XX
 PD 17-OCT-2000.
 XX
 PF 20-FEB-1998; 98US-00026985.
 XX
 PR 21-FEB-1997; 97US-0038664P.
 PR 22-JAN-1998; 98US-0074330P.
 XX
 PA (GETH) GENENTECH INC.
 PI Presta LG, Leong SR, Gonzalez TN;
 DR WPI; 2000-686027/67.
 XX
 PT Humanized anti-interleukin 8 monoclonal antibody variant useful for
 PT creating inflammatory disorders, such as adult respiratory distress
 PT syndrome, hypovolemic shock and ulcerative colitis.
 XX
 PS Disclosure; Col 143-144; 240pp; English.
 XX
 CC The present invention provides a number of humanised monoclonal anti-IL-8
 CC antibodies which can be used in the diagnosis and treatment of
 CC inflammatory disorders, including adult respiratory distress syndrome,
 CC septic shock, multiple organ failure, bacterial pneumonia and
 CC inflammatory bowel disease. The present sequence encodes one of the
 CC antibodies of the invention
 XX
 SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 1,55e-81 Length: 714
 Score: 1017.00 Matches: 194
 Percent Similarity: 96.3% Conservative: 12
 Best Local Similarity: 90.7% Mismatches: 8
 Query Match: 91.1% Indels: 0
 DB: 3 Gaps: 0
 US-10-635-908-15 (1-214) x AAC65491 (1-714)
 QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
 DB 70 GATATGTCATGACACAGTCTCAAAATTCATCTCCACATAGAGACAGCGGTACG 129
 QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTPrpYngInlyPro 40

```

DB      130 GTACCTGCAAGGCCGATGATGAGTGGGACTAATGAGCCGTGATCAACAGAAACCA 189
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      190 GGGCAATCTCCAAACACATGATTTACTGTCATCTCAGCGTACAGTGGAGTCCCTGAT 249
      61 ArgPhe|Thr|Gly|Ser|Gly|Ser|Gly|Thr|Asp|Phe|Thr|Leu|Thr|Leu|Ser|Asn|Met|Gln|Ser 80
      250 CGCTTACAGGCGATGATCTGGGACAGATTTACCTCACCATCAGCAGCATGTCAGTCT 309
      81 Glu|Asp|Leu|Ala|Asp|Phe|Phe|Cys|Gln|Gln|Thr|Ser|Asn|Tyr|Pro|Tyr|Phe|Gly|Gly 100
      310 GAAGACTTGCGACACTATTTCTGTCAGCATATTAACATCATCTCTCAGCTTCGGTCCCT 369
      101 G|Y|Thr|Lys|Leu|Gln|Leu|Lys|Arg|Thr|Val|Ala|Ala|Pro|Ser|Val|Phe|Ile|Phe|Pro|Pro 120
      370 GGGACCAAGCTGAGCTTCGAAAGCTGCTGGCTGACCATCTGCTTCTTCACTTCCGCCA 429
      121 Ser|Asp|Gln|Gln|Leu|Lys|Ser|Gly|Thr|Ala|Ser|Val|Val|Cys|Leu|Leu|Asn|Asn|Phe|Tyr 140
      430 TCTGATGAGGCAAGTTGAATCTGGAATCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 489
      141 Pro|Arg|Glu|Ala|Lys|Val|Gln|Tyr|Lys|Val|Asp|Asn|Ala|Leu|Gln|Ser|Gly|Asn|Ser|Gln 160
      490 CCAGAGAGGCCAAAGTACAGTGGAGAGTGAATACGCCCTCCCATCGGGTAACTCCAG 549
      161 Glu|Ser|Val|Thr|Gln|Gln|Asp|Ser|Lys|Asp|Ser|Thr|Tyr|Ser|Leu|Ser|Thr|Leu|Thr 180
      550 GAGAGTGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 609
      181 Leu|Ser|Lys|Ala|Asp|Tyr|Gln|Lys|Lys|Lys|Val|Tyr|Ala|Cys|Glu|Val|Thr|His|Gln|Gly 200
      610 CTGAGCAAGCAGACTCGAGAAACCAAAAGTCTACGCCCTCGCAAGTCAACCTCAGAGC 669
      201 Leu|Ser|Ser|Pro|Val|Thr|Lys|Ser|Phe|Asn|Arg|Gly|Gln|Cys 214
      670 CTGAGCTCGCCCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT 711

```

RESULT 15

ABX63872 standard; DNA; 714 BP.

ABX63872;

25-FEB-2003 (first entry)

Mouse anti-IL-8 mAb 5.12.14 VL/human IgG1 light chain DNA.

Antibody: monoclonal antibody; 5.12.14; 664.2.5; interleukin-8; mAb;
 anti-inflammatory; respiratory; acute lung injury; polyethylene glycol;
 PEG; lung injury; adult respiratory distress syndrome; ARDS; asthma;
 inflammatory disease; inflammatory bowel disease; psoriasis; sclerosis;
 ischaemic reperfusion disorder; stroke; multiple sclerosis; meningitis;
 osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis;
 alcoholic hepatitis; cystic fibrosis; ds; mouse; human.

Mus sp.

Homo sapiens.

OS Synthetic.

OS Chimeric.

US6468532-B1.

22-OCT-2002.

20-JAN-1999;

22-JAN-1998;

20-FEB-1998;

24-JUL-1998;

24-JUL-1998;

PA (GENTH) GENENTECH INC.
 XX Hsai V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 PI WPL: 2003-138230/13.
 XX P-PSDB; AB013778.
 DR
 XX
 PT Treating acute lung injury in mammal by administering to mammal a 500 kD
 PT conjugate comprising F(ab')₂ antibody fragment that binds to human
 PT interleukin-8, covalently attached to one or two polyethylene glycol
 PT molecules.
 XX
 XX Example D; Fig 19; 259pp; English.
 PS
 XX
 CC The invention relates to treating acute lung injury in a mammal,
 CC comprising administering to the mammal an effective amount of a conjugate
 CC of a single antibody fragment covalently attached to 1 or 2 polyethylene
 CC glycol (PEG) molecules, where the antibody fragment is a F(ab')₂
 CC comprising: (a) first chain that is either a light chain or a heavy chain
 CC ; (b) a first opposite chain that is either a heavy chain opposite the
 CC first light chain or a light chain opposite the first heavy chain; (c) a
 CC second chain that is either a light chain or a heavy chain; and (d) a
 CC second opposite chain that is either a heavy chain opposite the second
 CC light chain or a light chain opposite the second heavy chain; where every
 CC PEG molecule is covalently attached to a first cysteine residue in the
 CC first or second chain that would ordinarily form a disulphide bridge with
 CC a second cysteine residue in the first or second opposite chain, where
 CC the disulphide bridge is avoided by substitution of another amino acid
 CC residue for the second cysteine residue in the first or second opposite
 CC chain, where the F(ab')₂ comprises an antigen binding site that binds to
 CC human interleukin-8 (IL-8), and where the apparent size of the conjugate
 CC is at least about 500 kD. The antigen binding sites may be derived from
 CC murine monoclonal antibodies 5.12.14 or 664.2.5. The method is useful for
 CC treating lung injury, including adult respiratory distress syndrome
 CC (ARDS) in a mammal and inflammatory diseases (such as asthma,
 CC inflammatory bowel disease, psoriasis and sclerosis), ischaemic
 CC reperfusion disorders, stroke, autoimmune disease (e.g. Rheumatoid
 CC arthritis), alcoholic hepatitis, cystic fibrosis and many other diseases
 CC and disorders listed in the specification. The present sequence is a
 CC nucleic acid encoding a light or heavy chain variable region from one of
 CC the mouse interleukin-8 monoclonal antibodies fused to human IgG light or
 CC heavy chain sequences
 CC
 XX
 SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	714
Score:	1017.00	194
Percent Similarity:	96.3%	Conservative: 12
Best Local Similarity:	90.7%	Mismatch: 8
Query Match:	91.1%	Indels: 0
DB:	8	Gaps: 0

US-10-635-908-15 (1-214) x ABX63872 (1-714)

```

      1 Asp|Leu|Val|Met|Thr|Gln|Ser|Gln|Arg|Phe|Met|Ser|Thr|Val|Gly|Asp|Arg|Val|Ser 20
      70 GATATCTCATGACACAGTCTCAAAATTCATGCTCCACATCAGTACGAGAGAGAGTCCAGC 129
      21 Ile|Thr|Cys|Lys|Val|Asp|Ser|Gln|Asn|Val|Val|Ser|Ala|Val|Ala|Tyr|Tyr|Gln|Gln|Lys|Pro 40
      130 GTCACTCGCAAGGCCGATCAGAAAGTGGTGAATCATATATAGCTGCTGATCAACAGAAACCA 189
      41 G|yGlnSerPro|LysLeuLeu|Leu|Leu|Ser|AlaSer|AsnArg|Tyr|Thr|Gly|Val|Pro|Asp 60
      190 GGGCAATCTCCAAACACATGATTTACTGTCATCTCAGCGTACAGTGGAGTCCCTGAT 249
      61 ArgPhe|Thr|Gly|Ser|Gly|Ser|Gly|Thr|Asp|Phe|Thr|Leu|Thr|Leu|Ser|Asn|Met|Gln|Ser 80
      250 CGCTTACAGGCGATGATCTGGGACAGATTTACCTCACCATCAGCAGCATGTCAGTCT 309
      81 Glu|Asp|Leu|Ala|Asp|Phe|Phe|Cys|Gln|Gln|Thr|Ser|Asn|Tyr|Pro|Tyr|Phe|Gly|Gly 100

```

```
Db      310 GAAAGACTTGACACTATTCTGTCAGCAATATACATCTATCTCTCAAGTTGGTCTT 369
Qy      101 GYThrLysLeuGluLeuLysArgThrValAlaAlaProSerValPheIlePhePro 120
Db      370 GGGACCAAGCTGGAGCTGCGAAGAGCTGGCTGCACCATCTGTCTTCACTTCCGCCA 429
Qy      121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db      430 TCTGATGAGCAGCTTGAATCTGGAAGCTGCTTCTGTGTGTGCTGCTGAATAACTTCTAT 489
Qy      141 ProArgGluAlaLysValGlnTyrLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db      490 CCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATTAAGCCCTCCATCGGGTAACTCCCA 549
Qy      161 GluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db      550 GAGAGTGTCAACAGCAGGACAGCAAGACAGCACCCTACAGCCTCAGCAGCACCCTGAC 609
Qy      181 LeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200
Db      610 CTGAGCAAAAGCAGACTACGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGC 669
Qy      201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
Db      670 CTGAGCTCGCCCTCTCAAAAGAGCTTCAACAGGGGAGAGTGT 711
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Search completed: June 3, 2006, 04:12:54
Job time : 708.553 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 3, 2006, 04:13:15 ; Search time 5393.06 Seconds
(without alignments)
3328.373 Million cell updates/sec

Title: US-10-635-908-15
Perfect score: 1116
Sequence: 1 DIVTOSQSFMTTGVDRVS.....EYTHGLSSPVTKSFNRGEC 214

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %
Listing first 45 summaries

Command line parameters:
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-O=/abs/ABSWEB.spool/US10635908/runat_02062006_104216_10273/app_query.fasta_1
-DB=EST -OPMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h
-USR=US10635908 @CGN_1_1/986 @runat_02062006_104216_10273 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_hnc.*
7: gb_est2.*
8: gb_est7.*
9: gb_est8.*
10: gb_est9.*
11: gb_gsa1.*
12: gb_gsa2.*
13: gb_gsa3.*
14: gb_gsa4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	948	84.9	867	2	BG754732 602714301
2	944	84.6	856	2	BG758881 602713278
3	933.5	83.6	742	2	BG756519 602715662
4	932.5	83.6	903	3	BQ706785 AGENCOURT

5	932	83.5	810	4	CB956774	CB956774 AGENCOURT
6	932	83.5	943	2	BF976230	BF976230 602245105
7	931	83.4	964	3	BQ706786	BQ706786 AGENCOURT
8	928	83.2	774	4	BX336281	BX336281 AGENCOURT
9	926	83.0	925	3	BQ707105	BQ707105 AGENCOURT
10	925	82.9	803	4	CB958596	CB958596 AGENCOURT
11	924	82.8	716	2	BG755921	BG755921 602716389
12	923	82.7	750	2	BG755394	BG755394 602713951
13	923	82.7	854	2	BG755490	BG755490 602713864
14	922	82.6	1017	3	BQ056652	BQ056652 AGENCOURT
15	922	82.6	1047	3	BQ059853	BQ059853 AGENCOURT
16	922	82.6	1047	3	BQ063090	BQ063090 AGENCOURT
17	922	82.6	1124	3	BQ055107	BQ055107 AGENCOURT
18	921.5	82.6	840	2	BG755337	BG755337 602714075
19	921	82.5	849	2	BG745589	BG745589 602723821
20	920.5	82.5	776	2	BG684027	BG684027 602635634
21	919	82.3	947	3	BQ706698	BQ706698 AGENCOURT
22	918.5	82.3	962	2	BM914405	BM914405 AGENCOURT
23	918	82.3	1019	2	BG745435	BG745435 602723793
24	917.5	82.2	785	2	BM008264	BM008264 603616896
25	917	82.2	815	2	BG759762	BG759762 602711162
26	916	82.2	1048	3	BQ065573	BQ065573 AGENCOURT
27	916	82.1	875	2	BG685868	BG685868 602637982
28	915	82.0	667	1	AV651251	AV651251 AGENCOURT
29	914.5	81.9	744	2	BG686771	BG686771 602650742
30	914.5	81.9	1041	3	BQ072483	BQ072483 AGENCOURT
31	914	81.9	793	4	CB956343	CB956343 AGENCOURT
32	914	81.9	854	4	BX397739	BX397739 AGENCOURT
33	914	81.9	901	2	B1518472	B1518472 603062181
34	913	81.8	1065	3	BQ061622	BQ061622 AGENCOURT
35	911.5	81.7	729	2	BG685280	BG685280 602637190
36	911	81.6	721	2	BG686441	BG686441 602638377
37	911	81.6	727	2	BG684242	BG684242 602638574
38	911	81.6	728	2	BG757337	BG757337 602715342
39	910.5	81.6	1030	3	BQ711412	BQ711412 AGENCOURT
40	910	81.5	994	3	BQ711273	BQ711273 AGENCOURT
41	910	81.5	914	3	BQ707157	BQ707157 AGENCOURT
42	910	81.5	971	3	BQ706202	BQ706202 AGENCOURT
43	910	81.5	1013	3	BQ642324	BQ642324 AGENCOURT
44	909	81.5	1016	3	BQ065254	BQ065254 AGENCOURT
45	909	81.5	1018	3	BQ065739	BQ065739 AGENCOURT

ALIGNMENTS

RESULT 1
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DEFINITION mRNA sequence.
ACCESSION BG754732
VERSION BG754732.1 GI:14065385
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 867)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LNCM1702 row: a column: 02
High quality sequence stop: 805.

FEATURES
source

Location/Qualifiers
1..867
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4854409"
/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pOT87; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Size-selected for
average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 2,766-99 Length: 867
Score: 948.00 Matches: 179
Percent Similarity: 93.0% Conservative: 19
Best Local Similarity: 84.0% Mismatches: 15
Query Match: 84.9% Indels: 0
DB: 2 Gaps: 0
US-10-635-908-15 (1-214) x BG754732 (1-867)

QY 2 IIEVALMERThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSerIle 21
DB 88 ATCCAGTGAACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGAGTACACATC 147
QY 22 ThrCysLeuValAspSerGlnSerValValSerAlaValAlaATPTrpGlnGlnProGly 41
DB 148 ACTTGCCTGGCAGTACAGGCGCATTAAGCATGCTTTAGCCGTGATCAGAGAAACAGGG 207
QY 42 GlnSerProLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAspArg 61
DB 208 AAAGCTCTTAAGCTCTGATCTATGATGCTCCAGTTGGAAAGTGGGGGCTCTTAAGG 267
QY 62 PheThrGlySerGlySerGlyThrAspPheThrIleSerAsnMetGlnSerGlu 81
DB 268 TTACGGGGCGAGTGGATCTGGAGACAGATTCTACCTCAACATCGACGACCTGAA 327
QY 82 AspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 101
DB 328 GATTTTGCAACTTATTAATCTGCAACAGTTAATTAATTAATTAATTAATTAATTAATTA 387
QY 102 ThrLeuLeuGlnIleLeuValThrValAlaAlaProSerValPheIlePheProProSer 121
DB 388 ACCAAGGTGAGATCAACAACGACTGCTGACCACTGCTCTTCACTTCCCGCATCT 447
QY 122 AspGlnGlnLeuLeuSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrPro 141
DB 448 GATGAGACATTTAAATCTGAACTGCTCTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 507
QY 142 ArgGlnAlaLeuValGlnTrpValAspAsnAlaLeuGlnSerGlyAsnSerGlnGlu 161
DB 508 AGAGAGGCGCAAGATGAGTGAAGTGGATACGCCCTCAATCGGGTAACTCCAGAG 567
QY 162 SerValThrGlnGlnAspSerLeuAspSerThrTyrSerLeuSerSerThrLeuThrLeu 181
DB 568 AGGTGACAGAGAGGACAGCAAGACAGCACTACGCTCAGACAGCACTCAGACGCTG 627
QY 182 SerLeuAlaAspTyrGlnLeuIleIleValTyrAlaCysGlnValThrIleGlnGlyLeu 201
DB 628 AGCAAGACAGATCAAGAGAACACAAAGCTTACGCTTCGCAAGTCAACCATCAGAGGCTG 687
QY 202 SerSerProValThrTyrSerPheAsnArgTyrGlnCys 214
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RESULT 2

BG758881 856 bp mRNA linear EST 15-MAY-2001
LOCUS BG758881
DEFINITION 602713278F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853539 5',
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ACCESSION BG758881
VERSION BG758881.1 GI:14069534
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 856)
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gsapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCML699 row: 1 column: 20
High quality sequence stop: 746.

FEATURES

source

Location/Qualifiers
1..856

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4853539"
/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pOT87; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Size-selected for
average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 7,926-99 Length: 856
Score: 944.00 Matches: 180
Percent Similarity: 91.1% Conservative: 15
Best Local Similarity: 84.1% Mismatches: 19
Query Match: 84.6% Indels: 0
DB: 2 Gaps: 0
US-10-635-908-15 (1-214) x BG758881 (1-856)

QY 1 ASPILEVALMERThrGlnSerGlnArgPheMetSerThrValGlyAspArgValSer 20
DB 74 GACATCAAGATGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGTAAAGTACAG 133
QY 21 IIEThrCysLeuValAspSerGlnSerValValSerAlaValAlaATPTrpGlnGlnProGly 40
DB 134 ATCACTTGCAGGCGAGTCAAGACAGCACTATTTAATTTGATACAGCAAGAACCA 193
QY 41 GlyGlnSerProLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 194 GGAAGAGCCCTTAAGCTGATCTAATCGATCATTAATTTGAAACAGGGGCTCCATCA 253
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIleSerAsnMetGlnSer 80

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L16M2385 row: p column: 05
 High quality sequence stop: 697.
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:6216052"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7, site 1: XhoI; site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
 Alignment Scores:
 Pred. No.: 1,86e-97 Length: 903
 Score: 932.50 Matches: 179
 Percent Similarity: 92.1% Conservative: 19
 Best Local Similarity: 83.3% Mismatches: 16
 Query Match: 83.6% Indels: 1
 Gaps: 3

US-10-635-908-15 (1-214) x BQ706785 (1-903)

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QY 1 Aapllevalmethtginsertglnargphmetseththryalgllyaspargvalser 20
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DB 65 GACATCAATGACCAAGTCTCCTCTCTGTCGTCATCTAGACAGACAGATCACC 124
QY 21 IlethtCyalyaAlaserglnasenvalaserla---ValaLatrPyrglnlnly 39
   |||||
DB 125 ATCACTTGCGGCGAGTCAAGGTATTAGACAGAGCTGGTACCTGTATCAGAGAAA 184
QY 40 ProglYglNserProlyseuleulellyrserAlaserAsnArgYrThnglyValPro 59
   |||||
DB 185 CCAGGGAAGCCCTTAACCTCGATCTATGTCATCAAGTTCGCAAGTGGGGTCCA 244
QY 60 AspargPheThnglysergylsergylThnAspPheThrleuthrilleSeranMetGln 79
   |||||
DB 245 TCAGATTTCAGCGGCGAGTGTGAGACAGATTTCATCTCATCAGACACCTCGAG 304
QY 80 SerGluAspleuAlaAspPhePheCyrglnGlnTyrSerAsnTyrProTrpThrPheGly 99
   |||||
DB 305 CCGAAGATTTCGCACTTCTTTTGTCAACAGATTCCAGCTTCCTCAGACTTCGGC 364
QY 100 GlyglYthThlyseuululelyysargThValAlaAlaProserValPhelePhePro 119
   |||||
DB 365 GAGGAGCAAGGTGAGATCAACAGACAGTGGTGCACCACTGTTCATCTCCCG 424
QY 120 ProSerAspGlnGlnleuYsergylThnAlaserValAlaCysleuLeuAsnAspHe 139
   |||||
DB 425 CCATCTGATGAGAGATTGAATCTGGAACGCTCTGTTGTGTGCTCGCAATTAATCTC 484
QY 140 TyrProArgGlnAlaAlaYsValGlnTrpYsValAspAsnAlaLeuGlnSerGlyAsnSer 159
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DB 485 TATCCAGAGAGCCCAAGTACAGTGAAGTGAATTAACCCCTCAATCGGGTAACTCC 544

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QY 160 GlnGluSerValThrgluGlnAspSerLysAspSerThrTyrSerLeuSerSerThyleu 179
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DB 545 CAGGAGAGTGTACAGAGAGGACGACAGGACAGACACTTACAGCTTCAGCAGCACCCTG 604
QY 180 ThrLeuSerLysAlaAspTyrGlnYsIlyValAlaTyrAlaCysGluValThnArgln 199
   |||||
DB 605 AGCGTAGCAAGAACAGACTACGAGAAACCAAGTCTACGCTCGCAAGTCAACCATCAG 664
QY 200 GlyLeuSerSerProValThrlyserPheAsnArgGlyGlnCys 214
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DB 665 GGCTGAGCTCGCCCGTCAACAAAGACTTCAACAGGGAGAGTGT 709

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RESULT 5
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 LOCUS AGENCOURT.13666961 NIH_MGC.184 Homo sapiens CDNA clone
 DEFINITION IMAGE:30353409 5', mRNA sequence.
 ACCESSION CB956774
 VERSION CB956774.1 GI:30212891
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE
 1 (bases 1 to 810)
 NIH-MGC <http://mgc.nci.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 CDNA Library Preparation: CLOUTech Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

plate: NDCH154 row: b column: 10
 High quality sequence stop: 607.
 Location/Qualifiers
 1..810
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:30353409"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggcgcctggcc); Library is oligo-dT primed and directionally cloned. CDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATAGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCGCAGTGTG-(30)BA-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

FEATURES
 source

ORIGIN
 Alignment Scores:
 Pred. No.: 1,83e-97 Length: 810
 Score: 932.00 Matches: 178
 Percent Similarity: 92.5% Conservative: 20
 Best Local Similarity: 83.2% Mismatches: 16
 Query Match: 83.5% Indels: 0
 Gaps: 4

US-10-635-908-15 (1-214) x CB956774 (1-810)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
Db 108 GAAATGTATATACGAGTCTCCAGGCAACCTGTCTGTGTCTCCAGGGGAAAGATCACC 167
QY 21 IleThrCysLeuValAspSerGlnValSerAlaValAlaTPrpTyrGlnGlnPro 40
Db 168 CTCCTCGAGGGGCGAGTCAAGATGTAAACAATCTAGCCCTGTACCGAGCAAAACCT 227
QY 41 GlyGlnSerProIleuLeuIleTyrSerAlaSerAspAspTyrThrGlyValProAsp 60
Db 228 GGGCAGAGCTCCAGGCTCTCATCTATGTCATCCGCCAGGGGCACTGGTGTCTAAAC 287
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 288 AGGTTACAGTGGCGTGGTCTGGGACAGATTCACTCTACCTACCTACGACGCTGCACT 347
QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTPrpThrPheGlyGly 100
Db 348 GAGGATTTTGCAGTTATTAATCTGTCAGAGTATGAATAATGGCTCGAGCTCGGCA 407
QY 101 GlyThrIleLeuGlnIleIleArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 408 GGGACCAAGGTGAGATCAAAACGATGCTGCGACCATCTGTCTTCACTTCCGCCA 467
QY 121 SerAspGlnGlnLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 140
Db 468 TCTGATGACAGTGAATCTGGAATCTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTAT 527
QY 141 ProArgGlnAlaIleValGlnTPrpValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 528 CCCAGAGAGGCCAAAGATCAAGTGAAGTGAATACCCCTCCATGTGGTAACTCCACG 587
QY 161 GluSerValThrGlnGlnAspSerValAspSerThrTyrSerIleuSerSerThrLeuThr 180
Db 588 GAGAGTGTCAACAGGACGAGCAGCAGACGACGACCTTACGCTTACGACGACCTTACG 647
QY 181 LeuSerIleValAspTyrGlnIleValIleValIleValIleValIleValIleValIle 200
Db 648 CTGAGCAAGCAGACTCTCGAAGAACAACTTCACTTCACTTCACTTCACTTCACTTCA 707
QY 201 LeuSerSerProValThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 214
Db 708 CTGAGCTCGCCCGTCACAAAGAGCTTCAACGAGGAGAGTGT 749
RESULT 6 943 bp mRNA linear EST 22-JAN-2001
LOCUS BF976230
DEFINITION 602245105F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336225 5',
mRNA sequence.
ACCESSION BF976230
VERSION BF976230.1 GI:12343445
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo
1 (bases 1 to 943)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rudin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
cDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM1208 row: 1 column: 02
High quality sequence stop: 721.

FEATURES
source Location/Qualifiers
1..943
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4336225"
/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ALIGNMENT SCORES:
Pred. No.: 2,266-97 Length: 943
Score: 932.00 Matches: 178
Percent Similarity: 92.1% Conservative: 19
Best Local Similarity: 83.2% Mismatches: 17
Query Match: 83.5% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x BF976230 (1-943)

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Db 84 GACATCCAGATGACCCAGTCTCATCTCCGTCGTGATCTGTAGAGCAGAGTACAC 143
QY 21 IleThrCysLeuValAspSerGlnValSerAlaValAlaTPrpTyrGlnGlnPro 40
Db 144 ATCACTTGTGGCGAGTCAAGGATATTAGACAGCTGTACCTGTATCCAGCAAGAACCA 203
QY 41 GlyGlnSerProIleuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db 204 GGGAAAGCCCTTAAGTCTCGATCTATGTCATCCAGTTTGCAAAAGTGGGTCCTCA 263
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 264 AGGTTACAGCGGAGTGTATGAGACAGATTTCATCTCAACATCAAGCAGCTGCACT 323
QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTPrpThrPheGlyGly 100
Db 324 GAGGATTTTGCAGTCTTATTTGTCAACAGCTTATCCCTACACTTTGGCCAG 383
QY 101 GlyThrIleLeuGlnIleIleArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 384 GGGACCAAGCTGAGATCAAAACGATGCTGTCACATCTGTCTTCACTTCCGCCA 443
QY 121 SerAspGlnGlnLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 140
Db 444 TCTGATGACAGATGTGAATCTGAACTGCTGTGTGTGTGTGTGTGTGTGTGTGTAT 503
QY 141 ProArgGlnAlaIleValGlnTPrpValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 504 CCCAGAGAGGCCAAGATGACGTGAGAGTGTGATACCTTCCATGGGTAATCCACG 563
QY 161 GluSerValThrGlnGlnAspSerValAspSerThrTyrSerIleuSerSerThrLeuThr 180
Db 564 GAGAGTGTCAACAGGACGAGCAGACAGACGACCTTACAGCTTCAAGCAGCAGCTGAG 623
QY 181 LeuSerIleValAspTyrGlnIleValIleValIleValIleValIleValIleValIle 200
Db 624 CTGAGCAAGCAGCTCGAAGAACCAAACTTCACTTCACTTCACTTCACTTCACTTCA 683
QY 201 LeuSerSerProValThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 214
Db 684 CTGAGCTCGCCCGTCACAAAGAGCTTCAACGAGGAGAGTGT 725

RESULT	7
LOCUS	BQ06786
DEFINITION	BQ06786 AGNCORRUT_7976136 NIH_MGC_113 Homo sapiens cDNA IMAGE:6214887 5' UTRNA sequence.
ACCESSION	BQ06786
VERSION	BQ06786.1
KEYWORDS	GI:21845695 EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens <i>Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 964) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.</i>
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Email: csapbbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CNA Library Preparation: Rubin Laboratory
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LNCM2382 row: 0 column: 16
High quality sequence etop: 659.

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FEATURES
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                /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH_MGC Library."

```

ALIGNMENT	
ALIGNMENT SCORES:	
Pred. No.:	3,05e-97
Score:	931.00
Percent Similarity:	91.1%
Best Local Similarity:	82.2%
Query Match:	83.4%
DB:	3
US-10-635-908-15 (1-214) x BQ706786 (1-964)	

QY 1 AsplIeValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
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 DB 81 GACATCCAGATACCCAGTCTCCATCTCCCTCGTCGATCTGTGAGACAGAAATCC 140
 QY 21 IleThrCysLysAlaSerGlnAsnValSerAlaValAlaTrpTyrGlnGlnLysPro 40
 |||||
 DB 141 ATCATTCTGCGGGCAGATCAGAACATAGACACCTTTTAAATGGATATCAGAGAAACCA 200
 QY 41 GlyIlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
 |||||
 DB 201 GGGAGAGCCCAATCTCTGATCTTAACTGATCAGATTGGACAGAGGGGCTCCCATCA 260
 QY 61 ArgPheThrGlnLysGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
 |||||
 DB 261 AGTTTCATCTGGAGAGGATCTGGAGACAGATTTCATCTCACCATAGAGACAGTGGACCT 320

QY	8	GIuApLeuAlAlAspPhePhCysGlnGlnIlnYrSerSsnYrProTlPlnrPhedIyGly	100
		
Db	321	GGAGATTTTGCACTTACTTCTGTCAACAGCTTACAAATNCCCTCGAGCTTGGCGCA	380
QY	101	GIYThrLYsLeuGIuIlElEysRgThrValAlAlaProSerValPhelIephProP	120
		
Db	381	GGGACCAAGTGGAAATCAAGGAACTGGCTGCACACTGTGCTTCATCTTCCGCCCA	440
QY	121	SeTAspGIuGlnLeuLYsSerGIYThrAlAsSerValValCysLeuLeuAAsnAAsnPhETyr	140
Db	441	TCGAGAGACCAATTAAATCTGGAACTGCCTGTGTGTGTGCTCGTCAATAACTTCTAT	500
QY	141	ProxRGAlAlElEysValGIlnTrpLYsValAspAsnAlaLeuGlnSerGIYAsnSerGln	160
Db	501	CCCAAGAGAGCCAAAGTACAGTGGAAAGGTGATAAACCCTCCACATGGGTAATCTCCAG	560
QY	161	GIuSerValThrGIuGlnAspSerLYsAspSerThrTyrSerLeuSerSerThrLeuThr	180
Db	561	GAAGAGTCAAGACAGACGAGCAGAGACAGCACTACAGCCTCAGACACACCCCTGACG	620
QY	181	LeuSerLYsAlaAspTYrGIuLYsHilElyEysValYrAlaCysGIuValThrHileGlnGly	200
Db	621	CTGAGCAAAAGCAAGACTTACGAGAAACAAAAATCTTACGCTTGGAAAGTCCACCCATCAGGGC	680
QY	201	LeuSerSerProValThrLYsSerPheAsnArgGlyGluCys	214
Db	681	CTGAGCTCCCGCTCAACAAGAGCTTCAACAGGGGAGAGAGTCT	722

RESULT 8	774 bp	linear	EST 08-APR-2000
LOCUS	EX336281		
DEFINITION	EX336281 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA		
ACCESSION	EX336281		
VERSION	EX336281.2		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

1 (Bases 1 to 774)
Li, W. B., Gruber, C. I., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30341499.

Contact: Genoscope
Genoscope - Centre National de Séquençage
2 rue Gaston Cremlieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers
and enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of invitrogen. This sequence belongs to sequence cluster
1696.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna/s=C50BD1026DF110P1kc-1696.r>.

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FEATURES
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                /clone="CS01026YL22"
                /issue_type="PLACENTA COT 25-NORMALIZED"
                /clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /notes="1st strand cDNA was primed with a NotI-oligo (dT)
                    primer. Five prime end enriched, double-strand cDNA was
                    digested with Not I and cloned into the Not I and EcoR V
                    sites of the pCMVSPORT 6 vector. Library was normalized."

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Pred. No.:	5.01e-97	length:	778
Score:	928.00	Matches:	177
Percent Similarity:	92.1%	Conservative:	20
Best local Similarity:	82.7%	Mismatches:	17
Query Match:	83.2%	Indels:	0
DB:	4	Gaps:	0

US-10-635-908-15 (1-214) x BX336281 (1-774)

QY	1	aspIleValMe	trThngIn	SerGlna	ArgpHe	metSerThr	trVala	GI	aspArgVal	Ser	20																			
											21																			
Db	15	GACATCCAG	ATGACC	CACTTCC	ATCTTCC	GTCTG	CTGAT	CTG	AGAC	AGAGTAC	94																			
QY	21	Ile	trCys	Ly	sAla	SerGln	aAsn	Vala	Ser	aIa	al	trP	Y	Gln	In	Ly	Pro	40												
																		21												
Db	75	ATCATCTT	TCG	GGG	CGAG	TCA	GGG	GTAT	TG	CA	AG	CT	TG	TG	CA	AG	CT	134												
QY	41	Gly	In	Ser	Pro	Ly	s	Leu	Leu	I	Le	Ty	Ser	a	Le	Ser	a	Asn	Arg	Y	tr	th	G	ly	Val	Pro	asp	60		
																												41		
Db	135	GGGAAGCC	CTTA	AGCT	CTCT	CA	TAT	CTAT	CT	CA	AT	CT	CA	AT	CT	CA	AT	CT	CA	AT	CT	CA	AT	CT	CA	AT	CT	CA	194	
QY	61	Arg	pHe	tr	ng	I	ys	Ser	G	I	ys	Ser	G	I	ys	Ser	G	I	ys	Ser	G	I	ys	Ser	G	I	ys	Ser	G	80
																												61		
Db	195	AGGTTCA	GGG	CGA	CTG	CA	TCT	GGG	CA	CA	ATT	T	CA	CT	T	CA	CA	CT	T	CA	CA	CT	T	CA	CA	CT	T	CA	254	
QY	81	Glu	a	sp	Leu	a	asp	Phe	pHe	Cys	Gln	In	ty	r	Ser	a	en	Ty	r	Pro	T	Ph	r	Phe	G	ly	G	ly	100	
																												81		
Db	255	GAA	GAT	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	314	
QY	101	Gly	tr	ly	s	Leu	G	lu	I	le	Le	ys	Arg	tr	Val	a	I	a	a	P	ro	Ser	Val	Phe	I	e	Phe	Pro	120	
																												101		
Db	315	GGA	CA	CA	AG	T	GA	T	GA	A	T	CA	A	A	CA	CT	G	T	G	CT	G	CA	CA	T	C	T	G	T	374	
QY	121	Ser	a	sp	Arg	In	Leu	Leu	ys	Ser	G	I	ys	Ser	G	I	ys	Ser	G	I	ys	Ser	G	I	ys	Ser	G	I	ys	140
																												121		
Db	375	TCT	G	T	G	T	G	A	G	C	A	C	T	T	G	A	A	T	T	G	A	A	T	T	G	A	A	T	T	434
QY	141	Pro	Arg	G	lu	a	Leu	Val	a	G	In	T	Tr	ly	s	Val	a	Asp	a	sn	a	Leu	G	In	Ser	G	I	ys	Ser	160
																												141		
Db	435	CCCA	AG	AG	GG	CC	CA	AG	GT	CA	CT	CA	G	T	GA	AG	G	T	GA	AG	G	T	GA	AG	G	T	GA	AG	494	
QY	161	Glu	Ser	Val	Th	G	lu	G	lu																					

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LINTL at:
<http://image.llnl.gov>
Plate: LINC2473 row: 5 column: 10
High quality sequence stop: 647.
Location/Qualifiers

can be

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/mol_type="mRNA"
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/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming, directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGCGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

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ORIGIN	Alignment Scores:	1.le-96	Length:	925
Pred. No.:		926.00	Matches:	176
Score:		90.7%	Conservative:	18
Percent Similarity:		82.2%	Mismatches:	20
Best Local Similarity:		83.0%	Gaps:	0
Query Match:				
DB:				
US-10-635-908-15 (1-214) x BQ707105 (1-925)				
QY	1	AspIleValMetThrGlnSerGlnAlaArgHemetserrThrValaGlyAspArgValSer	20	
DB	71	GACATCCAGTTGACCCAGCTCCATCTCTCGTTCGATTTGTHGAGACAGACTCAC	130	
QY	21	IleThrCysLysAlaSerGlnAsnValaValSerAlaValaIleATrPYrGlnGlnLysPro	40	
DB	131	ATCATCTTCCCGGGCCAGTCAGGAGCATTTAGCAGTATTATTTGGCTCGGTATCAGCAAAACCA	190	
QY	41	GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThnGlyValProasp	60	
DB	191	GGGAAGACCCCAAGCTCCTGATCTTCTCGATCCACTTGGCAAGGGGGTCCCTTCA	250	
QY	61	ArgPheThrGlnYserGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer	80	
DB	251	AGGTCACAGGAGTGCATCTGAGATAGAAATTCATCTTCACATAGACAGCCTGCAGCT	310	
QY	81	GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAenTyrProTrpThrPheGlyGly	100	
DB	311	GAAAGATTGGAACTTATTACTGTCAACAACAGTAGTAATTACCCCTACACTTTTGGCCAG	370	
QY	101	GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro	120	
DB	371	GGGACTTAAGCTGGAATCAAGAACTGTGGCTGCACCATCTGTCTTCACTTCCCGCA	430	
QY	121	SerAspGlnGlnLeuLysSerGlyThrIleSerValValCysLeuLeuAsnAsnPheTyr	140	
DB	431	TGTGATGAGCAAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTCTCGAATTAATCTTAT	490	
QY	141	ProArgGlnAlaLysValaGlnTrpLysValaAspAsnAlaLeuGlnSerGlyAsnSerGln	160	
DB	491	CCCAAGAGAGCCCAAGATGACGTGAGAAAGGATTAACGCCCTTCATTCGGGTAACTCCAG	550	
QY	161	GlnSerValIleThnGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr	180	
DB	551	GAGAGTGTACAGAGACAGACAGCAAGCAGACACCTACAGCCTCAGACAGCACTGACG	610	
QY	181	LeuSerLysAlaAspTyrCylulysHisLysValTyrIlaCysGluValIleThnIleGlnGly	200	

Db 611 CTGACCAAGACAGACTACGAGAAACCAAGTCTAGCCTGCGAAGTCCATCAGGCGC 670

Qy 201 LeuSerSerProValThrLySerPheAnaArgLyGluCys 214

Db 671 CTGAGCTGCCCGCTCCACAAAGAGCTTCAACAGGGGAGACTGT 712

RESULT 10

CB958596 803 bp mRNA linear EST 29-APR-2003

LOCUS CB958596

DEFINITION AGENCOURT 1366622 NIH MGC 184 Homo sapiens cDNA clone

IMAGE:30354106 5', mRNA sequence.

CB958596

VERSION CB958596.1 GI:30214712

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 803)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

cDNA Library Preparation: Clontech Laboratories, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

http://image.llnl.gov

High quality sequence stop: 667.

Location/Qualifiers

1.803

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/db_xref="taxon:9606"

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/clone="IMAGE:30354106"

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/clone_lib="NIH MGC 184"

/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: S11 (ggccatcaggcc); Site_2: S11 (ggccgcctggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAAGCGCATTTATGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

ORIGIN

Alignment Scores:

Prod. No.: 1.18e-96 Length: 803

Score: 925.00 Matches: 175

Percent Similarity: 91.6% Conservative: 21

Best Local Similarity: 81.8% Mismatches: 18

Query Match: 82.9% Indels: 0

DB: 4 Gaps: 0

US-10-635-908-15 (1-214) x CB958596 (1-803)

Qy 1 AepIleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20

Db 90 GACATCCAGTTGACCCGATCCATCTCTCTGTCGACATCTAGAGAGACAGATCACC 149

Qy 21 IleThrCysIleValIleSerGlnMetValIleSerAlaValAlaIlePtyrGlnGlnLysPro 40

Db 150 TTCACCTGCGGGCCAGCTCAGCACTTAACAGTTATTTAGCTGATACGAAACGCCA 209

Qy 41 GlyIleSerProValLeuLeuIleTyrSerAlaSerAnaArgTyrThrGlyValProAsp 60

Db 210 GGGAAAGCCCTTAACCTCCTGATCTATGCTGCATCATTTTGCAAGAGGGGCTCCATCA 269

Qy 61 ArgPheMetGlySerGlySerGlyThrAspPheMetThrIleSerAnaMetGlnSer 80

Db 270 AGTTTCAGCGGAGAGATCCGGGACAGATTCACCTTACATACAGCAGCCTGACGCT 329

Qy 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAnaTyrProTyrThrPheGlyGly 100

Db 330 GAAGATTTTGCACTTATTAAGTCAACACACTTACGAATTAACCTCTCCTTCCGCGCA 389

Qy 101 GlyThrLeuLeuGluIleLeuValArgThrValAlaAlaProSerValPheIlePhePro 120

Db 390 GGGACCCAGGTGACATCAAGAACTGAGCTGACCACTGTCTTCACTTCCCGCCA 449

Qy 121 SerAspGluGlnLeuLeuSerGlyThrAlaSerValValCysLeuLeuAnaPheTyr 140

Db 450 TCTGATGAGCACTTGAATCTGAACTGCTCTGTGTGCTGCTGTAATTAATCTTAT 509

Qy 141 ProArgGluAlaIleValGlnTyrPheValAlaAspAnaAlaLeuGlnSerGlyAnaSerGln 160

Db 510 CCCAGAGAGCCAAAGTACAGTGAAGTGAATTAACGCTTCAATCGGCTAATCTCCAG 569

Qy 161 GluSerValThrGlnGlnAspSerIleValAspSerThrTyrSerLeuSerSerThrLeuThr 180

Db 570 GAGAGTGTACAGACAGACAGACAGAAAGACACACCTTACAGCTTCCAGCAGCCCTGAG 629

Qy 181 LeuSerIleValAspTyrGluIleValIleValIleValIleValIleValIleValIle 200

Db 630 CTGAGCAAGACAGACTACGAGAAACCAAGTCTAGCCTTGGAGATCCATCAGGCGC 689

Qy 201 LeuSerSerProValThrLySerPheAnaArgLyGluCys 214

Db 690 CTGAGCTGCCCGCTCCACAAAGAGCTTCAACAGGAGAGACTGT 731

RESULT 11

BG755921 716 bp mRNA linear EST 15-MAY-2001

LOCUS BG755921

DEFINITION 602716389F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856351 5',

RNA sequence.

CB955921

VERSION BG755921.1 GI:14066574

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 716)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

http://image.llnl.gov

High quality sequence stop: 714.

Location/Qualifiers

1.716

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FEATURES

source

/tissue_type="primary B-cells from tonsils (cell line)"
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/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	1,31e-96	Length:	716
Score:	924.00	Matches:	174
Percent Similarity:	89.7%	Conservative:	18
Best Local Similarity:	81.3%	Mismatches:	22
Query Match:	82.8%	Indels:	0
DB:	2	Gaps:	0

US-10-635-908-15 (1-214) x BG755394 (1-716)

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    GACATCCAGATGACCCAGTCTCTCCACCTGCTGCACTATCGAGACAGAGATCACC 133
DB 74
QY 21 IleThrCysIysAlaSerGlnAenValValSerAlaValAlaTrpTyrGlnGlnPro 40
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
    ATCATTGCGCGGCGCGATGAGAAATGCTTCTTGGTGGCTGGATACGAGAAACCA 193
DB 134
QY 41 GlyGlnSerProIysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
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    GGGAAAGCCCTTAACCTCATCTACATGCGCTTCTTACAAATAAGGGGTCGCCAGA 253
DB 194
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
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DB 254
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly 100
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DB 314
QY 101 GlyThrIysLeuGlnIleIysArgThrValAlaAlaProSerValPheIlePhePro 120
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DB 374
QY 121 SerAspGlnGlnLeuIysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
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    CCCAGAGAGCGCCAAAGTACAGTGGAGAGTGAATTAACCCCTCCATGCGGTAACTCCAG 553
DB 494
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DB 614
QY 201 LeuSerSerProValThrIysSerPheAsnArgGlyGlnCys 214
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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DB 674
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RESULT 12

BG755394 750 bp mRNA linear EST 15-MAY-2001
LOCUS BG755394 602713951F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854133 5',
DEFINITION mRNA sequence.

ACCESSION BG755394
VERSION BG755394.1 GI:14066047
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 750)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LLCM1701 row: e column: 14
High quality sequence stop: 711.
Location/Qualifiers

FEATURES

source

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/lab_host="DH10B (phage-resistant)"
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/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH_MGC library."
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ORIGIN

Alignment Scores:

Pred. No.:	1,83e-96	Length:	750
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Best Local Similarity:	80.8%	Mismatches:	18
Query Match:	82.7%	Indels:	0
DB:	2	Gaps:	0

US-10-635-908-15 (1-214) x BG755394 (1-750)

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DB 66
QY 21 IleThrCysIysAlaSerGlnAenValValSerAlaValAlaTrpTyrGlnGlnPro 40
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    GTCACCTTCCGCGGCGCATCAGGCGATGAGTAACTATTAGCTGATACGCAAAACCC 185
DB 126
QY 41 GlyGlnSerProIysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
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    GGGAAAGCCCTTAAGCTCTGATCTATATACATCCCTTTCGCAAAATGGGGTCCCATCA 245
DB 186
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
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    AGGTTACAGCGGCGATGATTCGGACAGAGTCACTTCAATCAGACGACCTGACGCT 305
DB 246
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly 100
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    GAAGATTTTGCACCTTATCTACTGTCAGCAACTTATGTTATACCTTTCACTTGGGCCCT 365
DB 306
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 3, 2006, 06:47:11 ; Search time 213.357 Seconds
(without alignments)
2815.117 Million cell updates/sec

Title: US-10-635-908-15

Perfect score: 1116
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Scoring table:

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	Fgapop 6.0 , Fgapext 7.0
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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	91.1	714	2	US-08-398-613A-27
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3	1017	91.1	714	2	US-08-398-611A-27
4	1017	91.1	714	2	US-08-398-611A-27
5	1017	91.1	714	2	US-08-491-334A-27
6	1017	91.1	714	3	US-09-027-449-24
7	1017	91.1	714	3	US-08-804-444A-24
8	1017	91.1	714	3	US-09-026-985-24

9	1017	91.1	714	3	US-09-121-952A-24	Sequence 24, Appl
10	1017	91.1	714	3	US-09-234-340A-24	Sequence 24, Appl
11	1017	91.1	714	3	US-09-355-014-24	Sequence 24, Appl
12	1017	91.1	714	5	US-09-726-258-24	Sequence 24, Appl
13	948	84.9	642	5	US-09-875-221B-127	Sequence 127, App
14	945	84.7	748	3	US-08-030-175-3	Sequence 3, Appl
15	943	84.5	660	3	US-08-952-235-3	Sequence 3, Appl
16	936	84.5	660	3	US-09-669-971-3	Sequence 29, Appl
17	936	83.9	974	3	US-09-859-053-29	Sequence 393, App
18	932	83.5	3819	3	US-09-042-353-393	Sequence 243, App
19	932	83.5	3819	3	US-08-758-417A-243	Sequence 1, Appl
20	931	83.4	1951	3	US-10-011-125A-1	Sequence 2, Appl
21	931	83.4	3300	4	US-10-020-786-2	Sequence 99, Appl
22	931	83.4	6072	2	US-08-908-469-99	Sequence 24, Appl
23	930	83.3	2178	2	US-08-463-587A-24	Sequence 2, Appl
24	930	83.3	2178	2	US-08-463-667A-2	Sequence 24, Appl
25	930	83.3	2178	7	US-08-923-854-24	Sequence 25, Appl
26	930	83.3	2178	7	PCT-US91-09133-25	Sequence 62, Appl
27	929	83.2	714	3	US-09-472-087-62	Sequence 4, Appl
28	928.5	83.2	4207	3	US-09-897-511A-7	Sequence 6, Appl
29	928.5	83.2	5732	3	US-09-897-511A-6	Sequence 7, Appl
30	928.5	83.2	9183	3	US-09-897-511A-7	Sequence 45, Appl
31	928	83.2	672	3	US-09-456-090A-45	Sequence 45, Appl
32	928	83.2	672	3	US-09-453-234-45	Sequence 50, Appl
33	927	83.1	5703	2	US-08-467-420A-50	Sequence 50, Appl
34	927	83.1	5703	2	US-08-470-110A-50	Sequence 50, Appl
35	927	83.1	5703	2	US-08-667-769A-50	Sequence 50, Appl
36	927	83.1	5703	2	US-08-940-371-50	Sequence 50, Appl
37	927	83.1	5703	3	US-08-637-647-50	Sequence 50, Appl
38	927	83.1	5703	3	US-10-700-740-50	Sequence 50, Appl
39	927	83.1	5703	7	PCT-US95-17082A-50	Sequence 50, Appl
40	926	83.0	654	7	PCT-US96-13152-1	Sequence 1, Appl
41	922.5	82.7	708	3	US-09-472-087-40	Sequence 40, Appl
42	922.5	82.7	708	3	US-09-472-087-56	Sequence 56, Appl
43	922.5	82.4	767	4	US-09-499-662-128	Sequence 128, App
44	920	82.4	931	3	US-09-049-672A-19	Sequence 19, Appl
45	918	82.3	705	2	US-08-488-376-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-398-613A-27
; Sequence 27, Application US/08398613A
; Patent No. 5677426
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,613A
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.

```
/
/ REGISTRATION NUMBER: 35,136
/ REFERENCE/DOCKET NUMBER: 874P1-3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1489
/ TELEFAX: 415/952-9881
/ TELEFAX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-398-612A-27

Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 0

US-10-635-908-15 (1-214) x US-08-398-612A-27 (1-714)

QY 1 AaplleValMerThrgInserGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 70 GATATGTCATATGACAGTCTCAAAATTCATGTCACATGAGAGACAGGCTCAGC 129

QY 21 lIethrCyLyAlaSerGlnAsnValValSerAlaValAlaATrPyGlnGlnInuysPro 40
DB 130 GTCACCTGCAAGGCCAGTCAAGATGGGACTCAATGAGCCGTGATCAAGAAACA 189

QY 41 GlyGlnSerProLyLeuLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAACACATGATTTACTGTCATCTTACCGGTACAGTGGAGTCCCTGAT 249

QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTACAGGCGAGTGTGAGACAGATTTACTCTCACATCCAGCCATGTCAGTCT 309

QY 81 GluAspLeuAlaAspPhePheCySerGlnGlnInuysSerAsnTyProTrpThrPheGly 100
DB 310 GAAGACTTGCCAGACATATTCTGTCAAGCATATACATCATCTCTCCAGTTCCGTCCT 369

QY 101 GlyThrLyLeuGlnIleLySerArgThrValAlaAlaProSerValIleIlePhePro 120
DB 370 GGGACCAAGCTGAGAGCTTCAAGAGCTGTGGCTGACCACTGTCTTCACTTCCGCCA 429

QY 121 SerAspGlnGlnInuysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTy 140
DB 430 TCTGATGAGCAGTTGAAATCTGGAATCTGCTTCTGTGTGCTGCTGCTGATTAATCTTCTAT 489

QY 141 ProArgGlnAlaLySerValGlnTrpLyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCCAGAGAGGCCAAAGATACAGTGAAGGTGATTAACGCCCTCCAAATCGGGTAACTCCAG 549

QY 161 GluSerValThrGlnGlnAspSerLyAspSerThrTySerLeuSerSerThrLeuThr 180
DB 550 GAGAGGTGTCAAGAGCAGCAGCAAGCAGCAGCACTTACAGCCTCAGCAGCCCTGAGAG 609

QY 181 LeuSerLyAlaAspTyGlyLySerAlaSerValAlaCysGlnValThrIleGlnGly 200
DB 610 CTGAGCAAAAGCAATCTACGAGAAACAAAGTCTTACGCTGCGAAGTCACTCCATCAGGGC 669

QY 201 LeuSerSerProValThrLySerPheAsnArgGlyGlnCys 214
DB 670 CTGAGCTCGCCCTGCAAAAGACTTCAACAGGAGGAGGTGT 711

RESULT 2
US-08-398-612A-27
Sequence 27, Application US/08398612A
Patent No. 5686070
GENERAL INFORMATION:
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/
/ APPLICANT: Doerehuk, Claire M.
/ APPLICANT: Fong, Sherman
/ APPLICANT: Hebert, Caroline Alice
/ APPLICANT: Kim, Kyung Jin
/ APPLICANT: Leong, Steven R.
/ TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
/ TITLE OF INVENTION: Treatment of Inflammatory Disorders
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/398,612A
/ FILING DATE: 01-MAR-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/398611
/ FILING DATE: 01-Mar-1995
/ APPLICATION NUMBER: 08/205864
/ FILING DATE: 03-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P0874P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-5530
/ TELEFAX: 415/952-9881
/ TELEFAX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Linear
US-08-398-612A-27

Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 0

US-10-635-908-15 (1-214) x US-08-398-612A-27 (1-714)

QY 1 AaplleValMerThrgInserGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 70 GATATGTCATATGACAGTCTCAAAATTCATGTCACATGAGAGACAGGCTCAGC 129

QY 21 lIethrCyLyAlaSerGlnAsnValValSerAlaValAlaATrPyGlnGlnInuysPro 40
DB 130 GTCACCTGCAAGGCCAGTCAAGATGGGACTCAATGAGCCGTGATCAAGAAACA 189

QY 41 GlyGlnSerProLyLeuLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
DB 190 GGGCAATCTCTTAAACACATGATTTACTGTCATCTTACCGGTACAGTGGAGTCCCTGAT 249

QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTACAGGCGAGTGTGAGACAGATTTACTCTCACATCCAGCCATGTCAGTCT 309

QY 81 GluAspLeuAlaAspPhePheCySerGlnGlnInuysSerAsnTyProTrpThrPheGly 100
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Db 310 GAAGACTGAGACATATTCTGTGAGCAATATAACATCTATCTCAGCTTCCT 369
QY 101 GYThrLysLeuGluLileysaGThrValAlaAlaProSerValPheIlePhePro 120
Db 370 GGGACCAAGCTGAGCTGACAGAGCTGGCTGCACCATCTCTTCACTTCCGCCA 429
QY 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTy 140
Db 430 TCTGATGAGCAGTTGAAATGTGAACTGCTTCTGTGTGTGCTGCTGAAATACTCTTA 489
QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 490 CCAGAGAGGCCAAAGTACAGTGGAGGTGATTAAGCCCTCCAAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGluGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180
Db 550 GAGAGGTGTCAAGAGCAGAGCAGACAGACAGCACTACAGCCTCAGACACACCTGACG 609
QY 181 LeuSerLysAlaAspTyrgLysLysLysValTyrrAlaCysGluValThrHisGlnGly 200
Db 610 CTGAGCAAGCAGACCTACGAAACACAAAGTCTAGCCCTGCGAAGTCAACCCATCAGGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
Db 670 CTGAGCTCGCCCTGACAAAGACTTCAACAGGGGAGAGTGT 711

RESULT 3

US-08-398-611A-27
Sequence 27, Application US/08398611A
Patent No. 5702946
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
TITLE OF INVENTION: of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,611A
FILING DATE: 01-Mar-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
US-08-398-611A-27

Alignment Scores:

Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: 2 Gaps: 0

US-10-635-908-15 (1-214) x US-08-398-611A-27 (1-714)

QY 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 70 GATATCGTATGACACAGTCTCAAAATTCATGTCACATCCATAGAGAGAGAGGATCAGC 129
QY 21 IleThrCysLysAlaSerGlnAsnValValSerAlaValAlaTrpTyrglnGlnLysPro 40
Db 130 GTCACCTGCAAGGCCAGTCAAGAAATGGGTACTCAATGTAAGTCCGTATCAACAGAAACA 189
QY 41 GlynSerProLysLeuLileysaGThrValAlaAlaProSerValPheIlePhePro 60
Db 190 GGGCAATCTCTTAAGCAGATCTGGAGACAGATTCTACCTCAACATCCAGTGCAGTGT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 250 CGCTTCACAGCAGGTGATCTGGAGACAGATTCTACCTCAACATCCAGTGCAGTGT 309
QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrrSerAsnTyrrProTrpThrPheGlyGly 100
Db 310 GAAGACTTGGCAGACATATTCTGTGCAATATAACATCTATCTCAGCTTCGCGTCT 369
QY 101 GYThrLysLeuGluLileysaGThrValAlaAlaProSerValPheIlePhePro 120
Db 370 GGGACCAAGCTGAGCTTCAAGAGCTGGCTGCACCATCTGTCTTCACTTCCGCCCA 429
QY 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAspPheTy 140
Db 430 TCTGATGAGCAGTTGAAATGTGAACTGCTTGTGTGTGCTGCTGAAATACTTAT 489
QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 490 CCAGAGAGGCCAAAGTACAGTGGAGGTGATTAAGCCCTCCAAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGluGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180
Db 550 GAGAGGTGTCAAGAGCAGAGCAGACAGACAGCACTACAGCCTCAGACACACCTGACG 609
QY 181 LeuSerLysAlaAspTyrgLysLysLysValTyrrAlaCysGluValThrHisGlnGly 200
Db 610 CTGAGCAAGCAGACCTACGAAACACAAAGTCTACGCCCTGCGAAGTCAACCCATCAGGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
Db 670 CTGAGCTCGCCCTGACAAAGACTTCAACAGGGGAGAGTGT 711

RESULT 4

US-08-396-851A-27
Sequence 27, Application US/08396851A
Patent No. 5707622
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,851A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitch, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874P1-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-396-851A-27

Alignment Scores:
Pred. No.: 1,86e-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 2

US-10-635-908-15 (1-214) x US-08-396-851A-27 (1-714)
QY 1 Aapllevalmethrinseginargphemetseththryvalglapargvalser 20
Db 70 GATATGCTATGACACAGCTCTCAAAATTCATGTCACATCAAGTACAGAGGCTCAGC 129
QY 21 IletHrCyLysAlaSerGlnaenValIserAlaValAlaTrpTyrgInglInylsPro 40
Db 130 GTACCTGCAAGGCGCTGCAAGATGGGTACTAATGAGCCGTGATCAACAGAAACCA 189
QY 41 GLYGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyTrhgIyValProasp 60
Db 190 GGGCAATCTCTTAAACACACTGATTTACTGTCTATCTTACCGGTACAGTGGAGTCCCTGAT 249
QY 61 ArgpheThrGlySerGlySerGlyThraApphethrLeuThrIleSerAsnMetGlnSer 80
Db 250 CGCTTCACAGGCGAGTGCATCTGGACAGATTTCACCTCACCCATCGACATGCGAGTCT 309
QY 81 GluAspLeuAlaAspPheCysGlnGlnTySerAsnTyProTrpThrPheGlyGly 100
Db 310 GAAGACTTGACACATATTTCTGTCAGCAATATTAATCTATCTCTCACGTTCCGTTCT 369
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
Db 370 GGGACCAAGCTGAGCTTGAAGAGCTGGCGGCGACCACTCTTCACTCTTCCCGCCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThraLaserValValCysLeuLeuAsnAsnPhetyr 140
Db 430 TCTGATGAGCAGCTTGAATCTGGAACCTCTTGTGTGTGCTGCTGTAATACTTCTAT 489
QY 141 ProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnInserGlyAsnSerGln 160
Db 490 CCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAAGCCCTCCAAATCGGGTAACTCCAG 549
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180
Db 550 GAGAGTGTCAACAGGACGACAGCAAGAGACAGCACTACAGCTTCAGGACCACTCTGAGC 609
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QY 181 LeuSerLysAlaAspTyrgIlyLysHisLysValIleCysGluValThrIseGlnGly 200
Db 610 CTGAGCAAGACGACATCAAGAGAAACAAAGCTACGCTGGAGATCAACCATCAGAGGC 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgIyGlyCys 214
Db 670 CTGAGCTGCGCCGTCAACAAAGAGCTTCAACAGGGAGAGACTGT 711

RESULT 5
US-08-491-334A-27
Sequence 27, Application US/08491334A
Patent No. 5874080
GENERAL INFORMATION:
APPLICANT: Hebert, Caroline A.
APPLICANT: Kabakoff, Rhona C.
APPLICANT: Moore, Mark W.
TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
Diseases and Asthma
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,334A
FILING DATE: 27-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: linear
US-08-491-334A-27

Alignment Scores:
Pred. No.: 1,86e-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 2

US-10-635-908-15 (1-214) x US-08-491-334A-27 (1-714)
QY 1 Aapllevalmethrinseginargphemetseththryvalglapargvalser 20
Db 70 GATATGCTATGACACAGCTCTCAAAATTCATGTCACATCAAGTACAGAGGCTCAGC 129
QY 21 IletHrCyLysAlaSerGlnaenValIserAlaValAlaTrpTyrgInglInylsPro 40
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Db      130  GTCACCTTCAGAGCCAGTCAGAAATGTGGTACTAAATGTAGCTCGTATCAAGAAACCA 189
      110  GlyInserProLyLeuLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
      190  GGGCAATCTCCATAAGCACTGATTTAACTGTCATCTCAACCGGATCAGTGGAGCTCGAT 249
      110  ArgPheThrGlySerGlySerGlyTyThrAspPheThrLeuThrIleSerLysMetGlnSer 80
      250  CGCTTCACAGGACAGTGAGTACTGGGACAGATTTCACTCACTCAACATCAAGATGACGCT 309
      110  GluAspLeuAlaAspPhePheCysGlnGlnTySerAsnTyProTrpThrPheGlyGly 100
      310  GAAAGCTTGCGAGACTATTCTGTACGAATATAATCACTATCTCTCACTTCGCTTCCGTC 369
      110  GlyThrTyLeuGlnIleLeuAsArgThrValAlaAlaProSerValPheIlePhePro 120
      370  GGGACCAAGCTGGAGCTTGAGAGAGCTGTGGTGGACCATCTGTCTTCACTTCCCGCCA 429
      110  SerAspGlnGlnLeuIleuysSerGlyTyThrAlaSerValValCysLeuLeuAsnAspPheTy 140
      430  TCTGATGAGCACTTGAAATCTGGAATCTGCTTCTGTGTGTGGCTGCTGTGAATTACTTAT 489
      110  ProArgGlnAlaIleValGlnTrpIleValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
      490  CCGAAGAGGCCCAAGATACAGTGAAGGTGATACGCCCTCCAAATCGGTAATCCAG 549
      110  GluSerValThrGlnIleAspSerLeuAspSerThrTySerLeuSerSerThrLeuThr 180
      550  GAGAGTGTCAACAGACGACGACACGACAGCAGCAGCACTCAACGCTTCAGCAGCACTGACG 609
      110  LeuSerTyLeuAlaAspTyGlnIleuysHisIleValTyThrAlaCysGlnValThrHisGlnGly 200
      610  CTGACCAAGCAGACTACAGAGAAACCAAAAGTCTACGCTCGCAAGTCAACCCATCAGGGGC 669
      110  LeuSerSerProValThrTySerSerPheAsnArgGlyGlnCys 214
      670  CTGAGCTCGCCCGCTCAAAAGACTTTCACAGGGGAGAGTGT 711

RESULT 6
US-09-027-449-24
; Sequence 24, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:

```

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/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P108SR3-2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-5530
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Linear
/
US-09-027-449-24

Alignment Scores:
Pred. NO.: 1,86e-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 3

US-10-635-908-15 (1-214) x US-09-027-449-24 (1-714)

QY 1 AsplilevImettrhGlnSerGlnrPhemSerThrValGlYsPaRgValSer 20
Db 70 GATATCGTCAAGACAGACTCTCAAAATTCATGTCACATCAGTGAAGACAGGGCTCAG 129
QY 21 lIethrCysLsAlaSerGlnAsnValISeralavalalatrPfyGlnGlnlyPro 40
Db 130 GTCACCTGTCAGAGCCAGTCAGAAATGTGGGTACTAATGTATGCTCGTATCAAGAAACCA 189
QY 41 GlynSerProLySleuLeuIlerySerAlaSerAsnArgTyrThrClYalProaP 60
Db 190 GGGCAATCTCTAAAGCACTGATTATCTGTCATCTCAACCGGTACAGTGAAGTCCCTGAT 249
QY 61 ArgPethrNglySerGlySerGlyThrAspPethrLeuThrIlEserAsnMetGlnSer 80
Db 250 CGCTTCACAGGACGATGATCTGGGACAGATTCCTTCACATCAGCCATGCGAGTCT 309
QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTrpThrPheGly 100
Db 310 GAAGCTTGGCAGACTATTCTGTGACGAAATTAACATTAATCCTCTCAGCTCGGTCT 369
QY 101 GlyThrlySleuGlnIleuYargThrValAlaIaProSerValPheIlePheProPro 120
Db 370 GGGACCAAGCTGAGACTTCGAAGACTGTGGCTGCGACCATCTGTCTTCACTTCCGCCA 429
QY 121 SerAspGlnGlnLeuLySerGlyThrAlaSerValValCyleuLeuAsnAsnPheTyr 140
Db 430 TCTGATGTAGCAAGTTGAAATCTGGAACTGCTTCTGTGTGTGCTCTGTAATTACTTCTAT 489
QY 141 ProArGgIuAlaIyValGlnTrpYsValaEaPmaAlaLeuGlnSerGlyAsnSerGln 166
Db 490 CCCAAGAGGCCAAAGCTACAGTGGAAAGGTGATTAAGCCCTCCATCCGGTAATCTCCAG 549
QY 161 GluSerValThrGlnGlnAspSerLyAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 550 GAGAGTGTCAACAGACAGACAGACAGACAGACAGACACTCAGCCTCAGACAGACCTGACG 609
QY 181 LeuSerLyAlaAspTyrGlyLysHslyYsValTyrAlaCyGgluValThrHsGlnGly 200
Db 610 CTGACCAAGCGACTTACAGAAACACAAAGCTTACGCTTGGCAAGTCAACCCATCAGGGC 669
QY 201 LeuSerSerProValThrLySerPheAsnArgGlyGlyCys 214
Db 670 CTGAGCTGCCCCGTCAACAAGACTTCAACAGGGAGAGTGT 711

RESULT 7
US-08-804-444A-24
; Sequence 24, Application US/08804444A
; Patent No. 6117980
; GENERAL INFORMATION:

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/ APPLICANT: Gonzalez, Tania N
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
/ NUMBER OF SEQUENCES: 61
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpacin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/804,444A
/ FILING DATE: 21-Feb-1997
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P1085
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/952-9881
/ TELEFAX: 650/225-5530
/
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Linear
/
/ US-08-804-444A-24
/
Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 0
US-10-635-908-15 (1-214) x US-08-804-444A-24 (1-714)
QY 1 AepIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGTCTCAAAAATTCATGTCCATCATGAGACAGAGGCTCACG 129
QY 21 IletHrCYeLYaAlaSerGlnAnValValSerAlaValAlaTrpTyrglnGlnLysPro 40
DB 130 GTACACTGCAAGCCAGTCAAGATGGGTACTAAATGTAATGCCGTGATCAACAGAAACCA 189
QY 41 GIVGInSerProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 190 GGGCAATCTCTCAACACCTGATTTACTGTCTACTCTACCGGTACAGTGGATGCTCTGAT 249
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAnMetGlnSer 80
DB 250 CGGTCACAGGGAGGTGATCTGGACAGATTTCATCTCACATCAGCATGCGCATGAGCATCT 309
QY 81 GIUAspLeuAlaAspPhePheCyGlnGlnGlnTyrsAsnTyrsProTrpThrPheGlyGly 100
DB 310 GAAGACTTGACAGACTTATTCGTCTGACGACATATATACATCATCTCTCAGCTTCCGCT 369
QY 101 GIYThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 370 GGGACCAAGCTGAGGCTTGACAGAGCTGGAGCTGACCATCTCTTCACTTCCGCGCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAnAnPheTyrs 140
DB 430 TCTGATGAGACAGTGTGAATCTGGAACCTGCTTCTGTGTGTGCTGCTGATTAATCTTAT 489
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QY 141 ProArgGluAlaLysValGlnTrpLysValAspAnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAACGCCCTTCACATCGGATTAATCCAG 549
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrsSerLeuSerSerThrLeuThr 180
DB 550 GAGACTGTCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 609
QY 181 LeuSerLysAlaAspTyrglyLysHisLysValTyraLysGluValThrHisGlnGly 200
DB 610 CTGAGCAAAAGCAGACTAGAGAGAAACACAAAGCTTACAGCTCGAAGTCACCATCAGGAG 669
QY 201 LeuSerSerProValThrLysSerPheAnArgGlyGlyCys 214
DB 670 CTGAGCTGCGCCGTCAAAAGCTTCAACAGGGAGAGTGT 711
/
/ RESULT 8
/ US-09-026-985-24
/ Sequence 24, Application US/09026985
/ Patent No. 6133426
/
/ GENERAL INFORMATION:
/ APPLICANT: Gonzalez, Tania R.
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
/ TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
/ NUMBER OF SEQUENCES: 72
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpacin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/026,985
/ FILING DATE: 20-Feb-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P1085R3-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/952-9881
/ TELEFAX: 650/225-5530
/
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Linear
/
/ US-09-026-985-24
/
Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
DB: Gaps: 0
US-10-635-908-15 (1-214) x US-09-026-985-24 (1-714)
QY 1 AepIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGTCTCAAAAATTCATGTCCATCATGAGACAGAGGCTCACG 129
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QY	21	llemhrCyvlysAlaSerGlnAsnValValSerAlaValAlaITrprYrGlnGlnYsPro	40
Db	130	GTCACTCTCAAGGCCAGTGTGAAATGTGGGTCTCAATATGTAAGCTGTGATACAGAAACCA	189
QY	41	GlyGlnSerProGlyLeuLeuLeuITrYSerAlaSerAsnArGTYrThrGlyValProAsp	60
Db	190	GGGCATCTCTTAAGACACTGATTTACTGTCTCATCTTACCGGTACAGTGGAGTCCCTGAT	249
QY	61	ArgPhehrnGlySerGlySerGlyYthrAspPheThrLeuThrITLeSerAsnMetGlnSer	80
Db	250	CGCTTCACAGCGCAGTGGATCTGGGACAGATTTCACCTCCACATCAGCATGTGCAGTCT	309
QY	81	GluAspLeuAlaAspPhePheCysGlnGlnITrYSerAsnTYrProITrPheGlyGly	100
Db	310	GAAGCTTGCGACACTATTCTGTGCGCAATATTAACATTAATCTTCACGTTGGTCT	369
QY	101	GlyThrYrLeuGlnITrLeYsArGrThrValAlaAlaProSerValPheITLePheProPro	120
Db	370	GGGACCAAGCTGTGAGCTTGCAGAGAGCTGTGGCTGCACATCTGTTCATCTTCCGGCA	429
QY	121	SerAspGlnGlnLeuYsSerGlyYThrAlaSerValValCysLeuLeuAsnAsnPheYr	140
Db	430	TCTGATGACAGATGTGAATCTGTGAATCTGCTTCTGTGTGTGGCTGTGCATATACCTTAT	489
QY	141	ProArGgluAlaIaIysValGlnITrPlyValAspAsnAlaITLeuGlnSerGlyAsnSerGln	160
Db	490	CCGAGAGAGGCCAAATATACAGTGGAGGTGGATTAAGCCCTCCAAATGTGGTAACTCCAG	549
QY	161	GluSerValIThrGlnGlnAspSerLyAspSerThTYrSerLeuSerSerIThrLeuThr	180
Db	550	GAGAGGTGTACAGACAGACAGACAGACAGACAGACACTTACAGCTTCAGACACACCTGACG	609
QY	181	LeuSerLyAlaAspTYrGlyYrShIaIysValITrAlaCysGluValIThrITGlnGly	200
Db	610	CTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCAGAAATCACCCATCAGGCG	669
QY	201	LeuSerSerProValIThrYrSerPheAsnArGrGlyGlnYs	214
Db	670	CTGAGCTCCGCCGTCAAAAGACTTCAACAGGGAGAGAGT	711

RESULT 9
 US-09-121-952A-24
 Sequence 24, Application US/09121952A
 Patent No. 645835
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc., HseI, Vanessa
 APPLICANT: Koumenis, Iphigenia
 APPLICANT: Leon, Steven R.
 APPLICANT: Presta, Leonard G.
 APPLICANT: Shahrokh, Zahra
 APPLICANT: Zapata, Gerardo A.
 TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
 TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/121,952A
 FILING DATE: 24-Jul-1998
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/074330
 FILING DATE: 22-JAN-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/075467
 FILING DATE: 20-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P1085R4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5530
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 714 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear

US-09-121-952A-24

Alignment Scores:	
Pred. No.:	1.86e-112
Score:	1017.00
Percent Similarity:	96.3%
Best Local Similarity:	90.7%
Query Match:	91.1%
DB:	3
	0
Length:	714
Matches:	19
Conservative:	12
Mismatches:	8
Indels:	0
Gaps:	0

US-10-635-908-15 (1-214) X US-09-121-952A-24 (1-714)

OY	1	Asp1LeValMetThrGlnSerGlnArgPheMetSerThrValGlnAspArgValSer	20
Db	70	GATATCTCTATGACACAGTCTCAAAATTCACATGTCACATCGAGACAGAGGTCAAG	120
OY	21	ILethrCysValAsaSerGlnAsnValSerAlaValAlaIleArgTyrGlnGlnAspPro	40
Db	130	GTCACTCGCAAGGCCATGATGATGCGGTACTAATGTAAGCCTGTATCAACAGAAACCA	180
OY	41	GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp	60
Db	190	GAGCAATCTCTTAAGACACTGATTTATCTGTATCTTCCGGTAAAGAGGAGTCTCTAT	240
OY	61	ArgPheThrGlnSerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer	80
Db	250	CGCTTCAACAGCAGGTGGATCTGGAGACAGATTTCACCTTCACATCAGCAGATGTGACGT	300
OY	81	GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly	100
Db	310	GAACACTTGGCAGACTTATCTGTGACGAATTAACATCTATTCCTCTCACGTTCCGGTCT	360
OY	101	GlyThrIlyLeuGlnIleValArgThrValAlaAlaProSerValPheIlePheProPro	120
Db	370	GGGACCAAGCTGGAGCTTCAMAGGCTGGCGCACCAATCGTCTTCACTTCCCGCA	420
OY	121	SerAspGlnGlnLeuLysSerGlyThrAlaSerValAlaCysLeuLeuAsnAsnPheTyr	140
Db	430	TCTGATAGCAGTTGAAATCTGGAACCTGCTTGTTGTGGCTGCTGAAATTAATCTTAT	480
OY	141	ProArgGlnAlaIlyValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln	160
Db	490	CCCAGAGAGGGCCAAAGTACAGTGGAGAGTGGAAAGCCCTCCAAATCGGGTAACTCCAG	540
OY	161	GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr	180
Db	550	GAGAGTGTCAAGACGACGACAGCAGCAGACGACCTACAGCTTACGACGACCCGTGACG	600
OY	181	LeuSerLysAlaAspTyrGlnLysHisIlyValTyrAlaCysGlnValThrHisGlnGly	200
Db	610	CTGAGCAAAAGCAGACTCGAGAAACCAAAAGTCTACGCTCGGAGAGTCAACCATCAGGCG	660
OY	201	LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys	224
Db	670	CTGAGCTGCCCCGTCAAAAGAGCTTCAACAGGGAGAGAGTGT	711

RESULT 10

US-09-234-340A-24
Sequence 24, Application US/09234340A
Patent No. 6468532
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heel, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-Feb-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
US-09-234-340A-24
Alignment Scores:
Pred. No.: 1,866-112 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 0
US-10-635-908-15 (1-214) x US-09-234-340A-24 (1-714)
QY 1 Aspllevalmethrnginserginaargphmetserthryvalgllyaspargvalser 20
DB 70 GATATGTCATGACACAGTCTCAAAAATTCATGTCCACATCAGTAGAGACAGGTCAGC 129
QY 21 IletthCyelysAlaserginaenValaIseValaValaIatTryPyngInglInlyPro 40
DB 130 GTCACCTCGACAGCCAGTCGATGAGATGCGTACTAATGTAAGCTCGTACCAAGAAACCA 189
QY 41 GlyInserProlylsleuLeuileTySerAlaSerAnargTyThrglyValProasp 60
DB 190 GGGCAATCTCTTAAGACACTGATTACTCGTCACTCCACCGGTACAGTGGAGTCCCTGAT 249

QY 61 ArgpnehrnglyserglyserglythraapphehrleuThrIleSeranmetcginser 80
DB 250 CGCTTCACAGGACGATGATCTGGACAGATTTCACCTCACATCAGCAGTGGAGTCT 309
QY 81 GluaSplleaAlaAapPhePheCysgInglIntySerAnTyProTrpThrPheglly 100
DB 310 GAAAGCTTGACAGACTATTCTGTGACGAATATACATCATTCCTCTCAGTTCCGTCC 369
QY 101 GlyThrlyLeuGluIlelyshgThrvAlaAlaProserValPheIlePheProPro 120
DB 370 GGGACCAAGCTGAGACTTCGAAGAGCTGGCTGACCTCTGTCTTCATCTTCCGCCA 429
QY 121 SerapglInglInleuLyserglythraIaservalValCysleuLeuAnanPheTy 140
DB 430 TCTGATGACAGCTGAAATCTGAACTGCTTGTTGTGTGCTGTGAATATCTTAT 489
QY 141 ProArgGluAlaLyvalGlnTrpLyValaAspaAlaLeuGlnserGlyansergIn 160
DB 490 CCCAGAGAGGCCAAAGTACAGTGAAGTGAATACGCCCTCAATCGGGTAATCTCCAG 549
QY 161 GluSerValThrGluGlnaAspSerlyAspSerThrTySerleuSerSerThrleuThr 180
DB 550 GAGAGTGTACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609
QY 181 LeuSerlyAlaAspTyrglyshlyshlyshlyshlyshlyshlyshlyshlyshly 200
DB 610 CTGAGCAAGACAGACTACGAGAAACACAAAGTCTACCTCGGAACTACCCATCAGGC 669
QY 201 LeuSerSerProValThrlySerPheAnargTyGlyCys 214
DB 670 CTGAGCTCGCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGT 711
RESULT 11
US-09-355-014-24
Sequence 24, Application US/09355014
Patent No. 6870033
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heel, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
FILING DATE: 21-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 base pairs

TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-355-014-24

Alignment Scores:

Pred. No.:	1,866-112	Length:	714
Score:	1017.00	Matches:	194
Percent Similarity:	96.3%	Conservative:	12
Best Local Similarity:	90.7%	Mismatches:	8
Query Match:	91.1%	Indels:	0
DB:	3	Gaps:	0

US-10-635-908-15 (1-214) x US-09-355-014-24 (1-714)

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QY 1 Aspl1eValMetThrgInSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGTCTCAAAAATTCATGCTCCATCAGTAGAGACAGGTCAGC 129
QY 21 IleThrCysValSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 130 GTACCTCGCAAGGCGACATGAGATGGGTAATATGATAGCTGGTATCAACAGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrglyValProAsp 60
DB 190 GGGCAATCTCTTAAGACATGATTTACTCGTCATCCACCGGTACAGTAGAGTCCCGAT 249
QY 61 ArgPheThrglySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGGACGATGATCTGGGACAGATTTCACTCTCACATCACACATGTGTCACT 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrPheGlyGly 100
DB 310 GAAGACTTGGCAGCTATTTCTGTGCACAAATATACATCTATCTCTCACGTTGCTCT 369
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePhePro 120
DB 370 GGGACCAAGCTGAGCTTCAGAGAGCTGGCTGCACATCTGCTTCATCTTCCGCCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 430 TCTGATGAGCAGTTGGAATCTGGAACGCTTCTGTGTGCTCCGCTGGAATATCTTAT 489
QY 141 ProArgGlnAlaLysValGlnTrpLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 490 CCCAGAGAGGCAAAAGTACAGTGAAGTGAATACGCCCTCCATGCGGTAACTCCAG 549
QY 161 GluSerValThrgInGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 550 GAGAGTCTCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609
QY 181 LeuSerLysAlaAspTyrGlyLysIleLysValIleValCysGluValThrHisGlnGly 200
DB 610 CTGAGCAAAAGCAGCTACGAGAAAACAAAGCTTACGCTCCGAAAGTCAACCATCAGG 669
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB 670 CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 711
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RESULT 12

US-09-726-258-24
Sequence 24 Application US/09726258

Patent No. 7005504

GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Genentech, Inc., Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shabrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/726,258

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/234,182

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/094003

FILING DATE: 24-JUL-1998

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R4-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 714 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Double

TOPOLOGY: Linear

US-09-726-258-24

Alignment Scores:

Pred. No.:	1,866-112	Length:	714
Score:	1017.00	Matches:	194
Percent Similarity:	96.3%	Conservative:	12
Best Local Similarity:	90.7%	Mismatches:	8
Query Match:	91.1%	Indels:	0
DB:	5	Gaps:	0

US-10-635-908-15 (1-214) x US-09-726-258-24 (1-714)

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QY 1 Aspl1eValMetThrgInSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
DB 70 GATATCGTCATGACACAGTCTCAAAAATTCATGCTCCATCAGTAGAGACAGGTCAGC 129
QY 21 IleThrCysValSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 130 GTACCTCGCAAGGCGACATGAGATGGGTAATATGATAGCTGGTATCAACAGAAACCA 189
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrglyValProAsp 60
DB 190 GGGCAATCTCTTAAGACATGATTTACTCGTCATCCACCGGTACAGTAGAGTCCCGAT 249
QY 61 ArgPheThrglySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 250 CGCTTCACAGGACGATGATCTGGGACAGATTTCACTCTCACATCACACACATGTGTCA 309
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrPheGlyGly 100
DB 310 GAAGACTTGGCAGCTATTTCTGTGCACAAATATACATCTATCTCTCACGTTGCTCT 369
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePhePro 120
DB 370 GGGACCAAGCTGAGCTTCGAAAGAGCTGGCTGCACATCTGCTTCATCTTCCGCCA 429
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
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DB 430 TCTGATGACGACGTGAATCTGAATCTCTTCTGTGTGTCTGTCTGAATTAATCTTCTAT 489
QY 141 ProATGJUALALyValGIntRPLYsValAAsPaAnaLLeuGInserGlyAnsSerGln 160
DB 490 CCCAAGAGGCCAAAGTACAGTGAAGGTGAATACGCCCTCCAAATCCGGGTAACTCCGAG 549
QY 161 GUSerValThrGluGlnAspSerLyAspSerThrTySerLeuSerSerThrLeuThr 180
DB 550 GAGAGTGTACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 609
QY 181 LeuSerLyAlAspTyGluLySerHisLyValTYRAlaCyGluValThrHisGlnGly 200
DB 610 CTGAGCAAGCAGACTACAGAAACACAAAGTCTACGCTCGGAATCCATCCATCAGGCC 669
QY 201 LeuSerSerProValThrLySerPheAnaArgGlyGlyCys 214
DB 670 CTGAGCTGCCCCGTCAACAAAGAGCTTCAACAGGGAGAGTGT 711
RESULT 13
US-09-875-221B-127
Sequence 127, Application US/09875221B
Patent No. 7012135
GENERAL INFORMATION:
APPLICANT: Achwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0089
CURRENT APPLICATION NUMBER: US/09/875,221B
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: GB0013810.7
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 127
LENGTH: 642
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Grafted light chain for fab and modified fab
US-09-875-221B-127
Alignment Scores:
Pred. No.: 3,02e-104 Length: 642
Score: 948.00 Matches: 183
Percent Similarity: 92.1% Conservative: 14
Best Local Similarity: 85.5% Mismatches: 17
Query Match: 84.9% Indels: 0
Gaps: 0
US-10-635-908-15 (1-214) x US-09-875-221B-127 (1-642)
QY 1 AspIleValIleThrGlnSerGlnAspPheMetSerThrThyValGlyAspArgValSer 20
DB 1 GACATTCGAATGATGACCCAGCCATCCAGCTGACGATCTAGAGAGCCCGGTCACC 60
QY 21 IleThrCyelyAlaSerGlnAenValValSerAlaValAlaIleThrTyGlnGlnLysPro 40
DB 61 ATCACTTGTAAACCCGATCGAAGCGTAGAGTAACTAAGTAACTCGGTATCGCAAAACCA 120
QY 41 GJGInSerProLyLeuLeuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
DB 121 GGTAAGCCCAAAAGCCCTCATCTACAGTGGCTTCTCTATATGTGTGTACCATAC 180
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerPheMetGlnSer 80
DB 181 AGGTTTCAGCGGATCCCGTAGTGTACTGATTTCAACCTTCAGATCAGTACCTCCAGCCA 240
QY 81 GluAspLeuAlaAspPhePheGlyGlnGlnTySerAsnTyProTrpThrPheGlyGly 100

DB 241 GAAAGTTTCGCCACTTATTAAGTACAGTAACTTAACATCTTACCACTCATTCCGTGAG 300
QY 101 GlyThrLyLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 301 GGTAATTAAGTGAATCAAAAGTACGATGAGCGGCCCATCTGTCTTCACTTCCCGCCA 360
QY 121 SerAspGluGlnLeuLysSerGlyThrAlaSerValValCyleuLeuAsnAsnPheTyR 140
DB 361 TCTGATGACGACATTAAATCTGAACCTGCTGTGTGTGTCTGTCTGAATTAATCTTCTAT 420
QY 141 ProATGJUALALyValGIntRPLYsValAAsPaAnaLLeuGInserGlyAnsSerGln 160
DB 421 CCCAAGAGGCCAAAGTACAGTGAAGGTGAATACGCCCTCCAAATCCGGGTAACTCCGAG 480
QY 161 GUSerValThrGluGlnAspSerLyAspSerThrTySerLeuSerSerThrLeuThr 180
DB 481 GAGAGTGTACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540
QY 181 LeuSerLyAlaAspTyGluLySerHisLyValTYRAlaCyGluValThrHisGlnGly 200
DB 541 CTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAATCCATCCATCAGGCC 600
QY 201 LeuSerSerProValThrLySerPheAnaArgGlyGlyCys 214
DB 601 CTGAGCTCACCAGTAAACAAAGAGCTTAAATAGAGGAGAGTGT 642
RESULT 14
US-08-030-175-3
Sequence 3, Application US/08030175
Patent No. 6757996
GENERAL INFORMATION:
APPLICANT: Gorman, Scott D.
APPLICANT: Clark, Michael R.
APPLICANT: Cobbold, Stephen P.
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSES: Rothwell, Pigg, Ernst & Kurz, P. C.
STREET: 555 13TH ST., NW Suite 701 East
CITY: Washington
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
COMPUTER: IBM AT compatible
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
SOFTWARE: Wordperfect 5.0 (Dos Text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175
FILING DATE: 17-MAY-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01578
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

FEATURE:
NAME/KEY: CDS
LOCATION: 41..742
US-08-030-175-3

Alignment Scores:
Pred. No.: 8,666-104
Score: 945.00
Percent Similarity: 91.1%
Best Local Similarity: 82.7%
Query Match: 84.7%
DB: 3

Length: 748
Matches: 177
Conservative: 18
Mismatches: 19
Indels: 0
Gaps: 0

US-10-635-908-15 (1-214) x US-08-030-175-3 (1-748)

QY 1 Aspl1eValmetThrgInserGlnArgPheMetSerThrValGlyAspArgValSer 20
DB 98 GACATCCAGATGAGCCGAGAGCCCAAGCAGCGCTGAGCGCGGTGACAGAGTGACC 157

QY 21 IleThrCysLysValAspSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 158 ATCACTGCTTACGAGTGAAGACATTACAGTATTACATGATGATCCAGAGAGCA 217

QY 41 GlyInSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 218 GGTAAAGCTCCAAAGCTGCTGATCTACATACATACATCTTCAAAATGGTGTGCCAAGC 277

QY 61 ArgPheThrGlySerGlySerGlyTyrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 278 AGATTTCAGCGGTAGCGGTAGCGGTACGACTTCACTTCCATCCAGACAGCCTCCAGCCA 337

QY 81 GlnAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrPheGlyGly 100
DB 338 GAGACATTCGCGCTTACTACTGCTCCAAAGATTAACATTAATCCGTGAGCTTGGGCAA 397

QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaIleProSerValPheIlePheProPro 120
DB 398 GGGACCAAGGTGGAATCAAAAGAACTGGCTGACCATCTGCTTCACTTCCGCCCA 457

QY 121 SerAspGlnGlnLeuLysSerGlyTyrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 458 TCTGATGAGCAGTGAATCTGAACTGCACTCTGTTGTGCTGCTGAAATTAACCTTCTAT 517

QY 141 ProArgGlnAlaLysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 518 CCCAGAGAGCCCAAGTACAGTGAAGGTGATTAACCCCTCCATCCGGTAATCTCCAG 577

QY 161 GlnSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 578 GAGAGTGTCAAGAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 637

QY 181 LeuSerLysAlaAspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGly 200
DB 638 CTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCTCGAAGTCAACCATCAGAGGC 697

QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys 214
DB 698 CTGAGCTGCGCGTCAAAAGCTTCAACAGGGAGAGTGT 739

RESULT 15
US-08-952-235-3
Sequence 3, Application US/08952235
Parent No. 6207152
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
APPLICANT: Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
TITLE OF INVENTION: Antagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460368
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-952-235-3

Alignment Scores:
Pred. No.: 1,256-103
Score: 943.00
Percent Similarity: 92.3%
Best Local Similarity: 80.9%
Query Match: 84.5%
DB: 3

Length: 660
Matches: 178
Conservative: 25
Mismatches: 11
Indels: 6
Gaps: 1

US-10-635-908-15 (1-214) x US-08-952-235-3 (1-660)

QY 1 Aspl1eValmetThrgInserGlnArgPheMetSerThrValGlyAspArgValSer 20
DB 1 GACATTAATGATGTCCTCACTCATCTCCCTCACTGTCAGTGTGAGAGAGGATTAAT 60

QY 21 IleThrCysLysValAspSerGlnAsnValVal-----SerAlaValAla 34
DB 61 GTGAGCTGCAAGTCCATCACTGCTCTTTATATATAGTACAGTCAAGAACTACTTGCC 120

QY 35 TrpTyrGlnGlnLysProGlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArg 54
DB 121 TGTATCCAGAGAAACAGAGTCACTTCTTAATCTGATTAATCTGGGATTCACATGAG 180

QY 55 TyrThrGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuThr 74
DB 181 GAATCTGGGGTCCCTGATCGCTTACAGGAGTGAATCTGGAGACAGATTTCACTTCACC 240

QY 75 IleSerAsnMetGlnSerGlnAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyr 94
DB 241 ATCAACAGTGTGAAGGTGAGCAGACTGCGAGTTATTAATCTGACAAATATTATGCGCAT 300

QY 95 ProTyrThrPheGlyGlyGlyThrLysLeuGlnIleLysArgThrValAlaIleProSer 114
DB 301 CCGTGAAGCTTCCGTGAGAGCAGCAAAAGTGAATCAAAAGCAGCAGTGTGACACACT 360

QY 115 ValPheIlePheProProSerAspGlnGlnLysSerGlyThrAlaSerValValCys 134
DB 361 GCTTCACTTCCCGCATCTGATGACAGTGAATTAATCTGGAATGCTGCTGTGTGTC 420

QY 135 LeuLeuAsnAsnPheTyrProArgGlnAlaLysValGlnTyrLysValAlaAspAsnAlaLeu 154
DB 421 CTGCTGAATTAATCTTATCCAGAGAGCCAAAGTACAGTGAAGGTGATTAACCCCTTC 480

QY 155 GlnSerGlyAsnSerGlnGlnLysValThrGlnGlnAspSerLysAspSerThrTyrSer 174

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Db      481 ||||| 540
          CATTGGGTAAGTCCAGAGAGTGTCAAGACAGAGACAGACAGACCTTACAGC
Qy      175 LeuSerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisIleValTyrAlaCys 194
          |||||
Db      541 CTCACAGACACCTCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTTACGCTTC 600
          |||||
Qy      195 GluValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
          |||||
Db      601 GAAGTCACCCATCAAGGCTGAGCTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 660
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Search completed: June 3, 2006, 06:53:38
Job time : 219.357 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 3, 2006, 06:54:05 ; Search time 1471.01 Seconds
(without alignments)
2681.378 Million cell updates/sec

Title: US-10-635-908-15

Perfect score: 1116
Sequence: 1 DVTMTQSGQFMSTVTGDRVS.....EYTHQGLASPTVKSFNRGEC 214

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSWB.spool/US10635908/runat_02062006_104222_10380/app_query.fasta-1
-DB=Published Applications NA Main -QMT=fastap -SUFFIX=rnbpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS-human0.cdt -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs02h
-USER=US10635908.@CGN 1.1 2326 @runat_02062006_104222_10380 -NCPU=6 -ICPU=3
-NRM MAMP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-NARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

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2: /EMC_Celerra_SIDS3/prodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/prodata/2/pubpna/US09_PUBCOMB.seq:*
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11: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10I_PUBCOMB.seq:*
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14: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11C_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11D_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11E_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1017	91.1	714 3	US-09-726-258-24 Sequence 24, Appl

2	1017	91.1	714	16	US-11-258-232-24	Sequence 24, Appl
3	977.5	87.6	699	13	US-11-020-508-14	Sequence 14, Appl
4	964	86.4	862	16	US-11-218-813-129	Sequence 129, App
5	964	86.4	12514	9	US-10-714-000-16	Sequence 16, Appl
6	964	86.4	12514	9	US-10-715-270-4	Sequence 4, Appl1
7	956	85.7	702	7	US-10-377-121-15	Sequence 15, Appl1
8	956	85.7	702	7	US-10-377-121-19	Sequence 19, Appl1
9	954.5	85.5	711	7	US-10-281-478A-55	Sequence 55, Appl1
10	954.5	85.5	711	7	US-10-275-180A-55	Sequence 55, Appl1
11	954.5	85.5	711	7	US-10-286-132A-55	Sequence 55, Appl1
12	948	84.9	642	3	US-09-949-559-127	Sequence 127, App
13	948	84.9	642	3	US-09-875-221A-127	Sequence 127, App
14	948	84.9	642	3	US-10-310-454-3	Sequence 3, Appl1
15	945	84.7	708	7	US-10-401-344-3	Sequence 3, Appl1
16	945	84.7	708	7	US-10-986-498-6	Sequence 112, Appl
17	944	84.6	642	9	US-10-914-015-112	Sequence 112, Appl
18	943	84.5	660	6	US-09-995-693-3	Sequence 3, Appl1
19	943	84.5	660	6	US-10-232-408-3	Sequence 3, Appl1
20	939.5	84.2	928	7	US-10-221-945-5	Sequence 5, Appl1
21	938	84.1	1710	15	US-10-291-265-99	Sequence 99, Appl1
22	938	84.1	1710	15	US-11-000-463-99	Sequence 99, Appl1
23	936	83.9	705	7	US-10-292-088-23	Sequence 23, Appl1
24	936	83.9	974	3	US-09-859-053-29	Sequence 29, Appl1
25	936	83.9	974	9	US-10-800-250-29	Sequence 29, Appl1
26	936	83.9	974	9	US-10-625-105-29	Sequence 29, Appl1
27	935	83.8	1404	7	US-10-291-265-663	Sequence 663, App
28	935	83.8	1404	15	US-11-000-463-663	Sequence 663, App
29	935	83.8	1711	10	US-10-901-011-5	Sequence 5, Appl1
30	935	83.8	9231	10	US-10-939-309-28	Sequence 28, Appl1
31	934	83.7	642	10	US-10-644-277-63	Sequence 63, Appl1
32	934	83.7	1477	9	US-10-728-420B-116	Sequence 116, App
33	934	83.7	1477	9	US-10-728-420B-117	Sequence 117, App
34	934	83.7	3300	9	US-10-764-428-24	Sequence 24, Appl1
35	933	83.6	711	10	US-10-910-901-11	Sequence 11, Appl1
36	932	83.5	645	8	US-10-408-901-35	Sequence 35, Appl1
37	932	83.5	3819	16	US-11-009-840A-243	Sequence 243, App
38	932	83.5	3819	16	US-11-009-878A-243	Sequence 243, App
39	932	83.5	3819	16	US-11-009-769A-243	Sequence 243, App
40	931	83.4	660	16	US-11-049-536-702	Sequence 702, App
41	931	83.4	660	16	US-11-199-739-702	Sequence 702, App
42	931	83.4	1911	16	US-10-011-125-1	Sequence 1, Appl1
43	931	83.4	3255	10	US-10-697-995-10	Sequence 10, Appl1
44	931	83.4	3255	10	US-10-697-995-10	Sequence 10, Appl1
45	931	83.4	3300	6	US-10-020-786-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-726-258-24
Sequence 24, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Komnents, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
NUMBER OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS


```
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/726,258
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/234,182
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/094003
/ FILING DATE: 24-JUL-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P1085R4-1A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-5530
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 714 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Linear
/
US-09-726-258-24

Alignment Scores:
Pred. No.: 2,14e-118 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 0

US-10-635-908-15 (1-214) x US-09-726-258-24 (1-714)
QY 1 Aapllevalmethrchlnserglnargphemetserthrthrvajllyapargvalser 20
DB 70 GATATGTCATGACACAGCTCAAAATTCATGTCACATCACTAGAGACAGGTCACG 129
QY 21 Iletnrcyalyealaserglnanvalvalseralvalatrrpyrglnglnlypro 40
DB 130 GTCACCTGCAAGGCCGCTGAGATGGGACTCAATGACCTGCTGATCAACGAAACCA 189
QY 41 Glylnserprolyseuleuiletyrseralaserasnargtyrthrjlyvalproasp 60
DB 190 GGGCAATCTCTTAACACACTGATTTACTGCTACCGGACGAGGAGTCCCTGAT 249
QY 61 Argphethrglyserglyserglythraapphetrleuthrllseeransmetglnser 80
DB 250 CGCTTACAGGCGAGTGCATCTGGACAGATTCTCACTCCACATCCATGTCAGTCT 309
QY 81 Gluaspleualaaaphephecysglnlntyrserasntyrprotrprrhphedgly 100
DB 310 GAAGACTTGCCACATATTTCTGTCAGCATATTAACATCATCTCTCAAGTTCGGTCT 369
QY 101 Glythrlvleuglnllyleuysargthrvalajalaproservalpheillephepro 120
DB 370 GGGACCAAGCTGAGCTTGCAGAGCTGTGGCTGCACCATCTGCTTCACTTCCGCCCA 429
QY 121 Seraspgluglnleuyserserjlythralaservalcysleuleuansanpheityr 140
DB 430 TCTGATGACAGCTGAAATCTGAACCTGCTTGTGTGCTGCTGCTGAATTAATCTTAT 489
QY 141 Proarglualalysvalglntrplyvalaspaasnalaleuglnserglyaanserjln 160
DB 490 CCCAGAGAGCCCAAGTACAGTGGAGGTGATTAACCCCTCCAAATCGGTAACTCCAG 549
QY 161 Gluservalthrjluglnaapserlyraspserthrtyrserleuenserthrleuthr 180
DB 550 GAAGTGTCTACAGACGACAGCAAGACAGACACCTTACAGCAGACACCTGAGACG 609
QY 181 Leuserlyealaaaptryrglulvghllevaltyralacysegluvalthrhlsglngly 200
```

```
DB 610 CTGACCAAGACGACTAGAGAAACAAAGTCTACGGCTGCACTACCATCAGGAC 669
QY 201 LeuserSerProvalThrlyseerPheasnarglyglycys 214
DB 670 CTGAGCTCGCCCGCTCAACAAAGAGCTTCAACAGGGAGAGGTGT 711

RESULT 2
US-11-259-232-24
/ Sequence 24, Application US/11259232
/ Publication No. US20060083683A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc., Heel, Vanessa
/ APPLICANT: Koumenda, Iphigenia
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Shantokh, Zahra
/ APPLICANT: Zapata, Gerardo A.
/ TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND USES OF SAME
/ FILE REFERENCE: P1085R6
/ CURRENT APPLICATION NUMBER: US/11/259,232
/ PRIOR FILING DATE: 2005-10-25
/ PRIOR APPLICATION NUMBER: US/09/489,394
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 60/116,787
/ PRIOR FILING DATE: 1999-01-21
/ NUMBER OF SEQ ID NOS: 72
/ SEQ ID NO 24
/ LENGTH: 714
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: Artificial Sequence
/ LOCATION: 1-714
/ OTHER INFORMATION: recombinant immunoglobulin
/
US-11-259-232-24

Alignment Scores:
Pred. No.: 2,14e-118 Length: 714
Score: 1017.00 Matches: 194
Percent Similarity: 96.3% Conservative: 12
Best Local Similarity: 90.7% Mismatches: 8
Query Match: 91.1% Indels: 0
Gaps: 0

US-10-635-908-15 (1-214) x US-11-259-232-24 (1-714)
QY 1 Aapllevalmethrchlnserglnargphemetserthrthrvajllyapargvalser 20
DB 70 GATATGTCATGACACAGCTCAAAATTCATGTCACATCACTAGAGACAGGTCACG 129
QY 21 Iletnrcyalyealaserglnanvalvalseralvalatrrpyrglnglnlypro 40
DB 130 GTCACCTGCAAGGCCGCTGAGATGGGACTCAATGACCTGCTGATCAACGAAACCA 189
QY 41 Glylnserprolyseuleuiletyrseralaserasnargtyrthrjlyvalproasp 60
DB 190 GGGCAATCTCTTAACACACTGATTTACTGCTACCGGACGAGGAGTCCCTGAT 249
QY 61 Argphethrglyserglyserglythraapphetrleuthrllseeransmetglnser 80
DB 250 CGCTTACAGGCGAGTGCATCTGGACAGATTCTCACTCCACATCCATGTCAGTCT 309
QY 61 Argphethrglyserglyserglythraapphetrleuthrllseeransmetglnser 80
DB 250 CGCTTACAGGCGAGTGCATCTGGACAGATTCTCACTCCACATCCATGTCAGTCT 309
QY 81 Gluaspleualaaaphephecysglnlntyrserasntyrprotrprrhphedgly 100
DB 310 GAAGACTTGCCACATATTTCTGTCAGCATATTAACATCATCTCTCAAGTTCGGTCT 369
QY 101 Glythrlvleuglnllyleuysargthrvalajalaproservalpheillephepro 120
DB 370 GGGACCAAGCTGAGCTTGCAGAGCTGTGGCTGCACCATCTGCTTCACTTCCGCCCA 429
QY 121 Seraspgluglnleuyserserjlythralaservalcysleuleuansanpheityr 140
DB 430 TCTGATGACAGCTGAAATCTGAACCTGCTTGTGTGCTGCTGCTGAATTAATCTTAT 489
```

Oy	141	ProarrglublalalyvalgintprrpysvalaaparralalenglSe-rglYamsSerGln	160
Db	490	CCCGAAGAGGCACAAAGTACAGTGAAGGTGATACGCCCTCCATCGGGTAACTCCAG	544
Oy	161	GluserValThrgluglnaPpserlYsaPserThYrSerleuserSerThreuthr	186
Db	550	GAGAGTGTCAcAGAGcAGcAGcACAGcAGcAGcACcCTACAGcCTcAGcAGcACcCTGAGc	601
Oy	181	leuserlYsaalaaPrrYrglulYrshlsYsValTYrAlaCYeGluValThrhInglnly	200
Db	610	CTGAGCAACACAGCTACAGAAACCAAGGCTTACGCTCGGAATCACCCATCAGGAC	661
Oy	201	leuserSerProvalThrlYsSerPheAemarglYlucYs	214
Db	670	CTGAGCTCGCCCTCAGCAAGAGCTTCACAGGGGAGAGTGT	711
RESULT 3			
US-11-020-508-14			
Sequence 14, Application US/11020508			
Publication No. US20050226865A1			
GENERAL INFORMATION:			
APPLICANT: CHANG, WESLEY			
APPLICANT: EATON, DAN L.			
APPLICANT: EBENS, ALLEN JR.			
APPLICANT: DE SAUVAGE, FREDERIC J.			
APPLICANT: FRANTZ, GRETCHEN			
APPLICANT: HONGO, JO-ANNE			
APPLICANT: KOEPFEN, HARTMUT			
APPLICANT: POLSON, ANDREW			
APPLICANT: SMITH, VICTORIA			
TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor or			
TITLE OR INVENTION: Hematopoietic Origin			
FILE REFERENCE: P5109R1-US			
CURRENT APPLICATION NUMBER: US/11/020,508			
CURRENT FILING DATE: 2004-12-21			
PRIOR APPLICATION NUMBER: PCT/US2004/038262			
PRIOR FILING DATE: 2004-11-16			
PRIOR APPLICATION NUMBER: US 10/989,826			
PRIOR FILING DATE: 2004-11-16			
PRIOR APPLICATION NUMBER: US 60/520,842			
PRIOR FILING DATE: 2003-11-17			
PRIOR APPLICATION NUMBER: PCT/US03/36298			
PRIOR FILING DATE: 2003-11-13			
PRIOR APPLICATION NUMBER: US 10/712,892			
PRIOR FILING DATE: 2003-11-13			
PRIOR APPLICATION NUMBER: US 10/643,795			
PRIOR FILING DATE: 2003-08-19			
PRIOR APPLICATION NUMBER: PCT/US03/25892			
PRIOR FILING DATE: 2003-08-19			
PRIOR APPLICATION NUMBER: US 60/426,847			
PRIOR FILING DATE: 2002-11-15			
PRIOR APPLICATION NUMBER: US 10/241,220			
PRIOR FILING DATE: 2002-09-11			
PRIOR APPLICATION NUMBER: PCT/US02/28859			
PRIOR FILING DATE: 2002-09-11			
Remaining prior Application data removed - See File Wrapper or PALM.			
NUMBER OF SEQ ID NOS: 17			
SEQ ID NO 14			
LENGTH: 699			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-11-020-508-14			
Alignment Scores:			
Pred. No.: 2,166-113			
Score: 977.50			
Percent Similarity: 94.4%			
Best Local Similarity: 88.8%			
Query Match: 87.6%			
DB: 13			
Length: 699			
Matches: 190			
Conservative: 12			
Mismatches: 11			
Indels: 1			
Gaps: 1			
US-10-635-908-15 (1-214) x US-11-020-508-14 (1-699)			

Qy	1	Asp1LeValMetThrGlnSerGlnAlaArgPheMetSerThrTrpValGlyAspArgValSer	20
Db	58	GATATTCGTGATGACCCAGTCTCATTAATTCATGTCACATCATAGTAGAGAACGGGTCCAGC	117
Qy	21	11eThrCysIysValAspSerGlnAsnValAspSerAlaValAlaTrpTyrGlnGlnIlyPro	40
Db	118	ATTCCTCGCAAGGCGACGACGAGATGTGGTCTGCTGTAAGCTGGTATCAACAGAACCA	177
Qy	41	GlyGlnSerProCysIleuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp	60
Db	178	GGACATTCCTCTAAACTACTATTAATTCG--GGATACCGGTACACTAGAGTCCCTGAT	234
Qy	61	ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer	80
Db	235	CGCTTCACTGGCAAGTGGATCTGGGACGATTTCACTTCCACATCAGCAGTGGCAGGCT	294
Qy	81	GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly	100
Db	295	GAAAGCCCTGGCATTTTATTTCTGTCAGCAACATTTAGTACTCCATTCAGTTCGGCTCG	354
Qy	101	GlyThrIlySerGluIleIleAspArgThrValAlaAlaProSerValPheIlePheProPro	120
Db	355	GGTACCAAGGTGAGATCAACAGACTGTGGCTGCACCATCTGTCTTCAATCTTCCGCCA	414
Qy	121	SerAspGlnGlnLeuIlySerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr	140
Db	415	TCGTATGACGAGTTGAATCTGGAACTGGCTTCTGTTGTGTGCTGCTGTAATACTTAT	474
Qy	141	ProArgGluAlaIlyValGlnTrpIlyValAspAsnAlaLeuGlnSerGlyAsnSerGln	160
Db	475	CCGAGAGGCGCCAAAGTACAGTGAAGGATACGCCCTCCAAATCGGGTAACTCCAG	534
Qy	161	GluSerValThrGlnGlnAspSerIysAspSerThrTyrSerLeuSerSerThrLeuThr	180
Db	535	GAGAGTGTCAAGACACAGACACGACAGACACCTACAGCTTCAGAGCACCCCTGACG	594
Qy	181	LeuSerIlySAlaAspTyrGlnIlyShiIlyValTyrAlaCysGluValThrHisGlnGly	200
Db	595	CTGACCAAGCAGACTACAGAAACAAAGTCTACGCTGGGAGTCAACCCATCAGGCGC	654
Qy	201	LeuSerSerProValThrIlySerSerPheAsnArgGlyGluCys	214
Db	655	CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	696
RESULT 4			
US-11-218-813-129			
/ Sequence 129, Application US/11218813			
/ Publication No. US20060062793A1			
GENERAL INFORMATION:			
/ APPLICANT: Webb, Iain J.			
/ APPLICANT: Horvath, Christopher J.			
/ TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC			
/ FILE REFERENCE: 10448-163005 US/11/218, 813			
/ CURRENT FILING DATE: 2005-09-02			
/ PRIOR APPLICATION NUMBER: PCT/US2004/006543			
/ PRIOR FILING DATE: 2004-03-03			
/ NUMBER OF SEQ ID NOS: 144			
/ SOFTWARE: FaastSeq for Windows Version 4.0			
/ SEQ ID NO 129			
/ LENGTH: 862			
/ TYPE: DNA			
/ ORGANISM: Artificial Sequence			
/ FEATURE:			
/ OTHER INFORMATION: Light chain variable and constant region of deus591			
/ NAME/KEY: CDS			
/ LOCATION: (151)..(849)			
US-11-218-813-129			
Alignment Scores:			

Pred. No.: 1.51e-111 Length: 862
Score: 964.00 Matches: 183
Percent Similarity: 93.5% Conservative: 17
Best Local Similarity: 85.5% Mismatches: 14
Query Match: 86.4% Indels: 0
DB: 16 Gaps: 0

US-10-635-908-15 (1-214) x US-11-218-813-129 (1-862)

```
QY 1 Aapllevalmetthrcinserglnargphmetserthrthrvaiqlvysparyvalser 20
DB 208 GACATCCAGATGACCCAGTCCCTCCATCCCTGATCCATCAGATGAGAGACAGGCTCACC 267
QY 21 IletthrcylvalaserglnasenvaiValserAlaValatPtyrtynglnlysp 40
DB 268 CTCACCTGTAAGCCAGTCAAGATGGGTGCTGCTGATGACTGCTATCAACAGAAACCA 327
QY 41 GlylnserProlyseuleuiletyrserAlaserAsnArgTyrthrclyValProap 60
DB 328 GGAACCTCTCTTAACCTACTGATTTATTGGGCTTCCACTCGGACACTGGAATCCTTACT 387
QY 61 Argpethrclyserglyserglythraepthrclythraepthrclythraepthrcly 80
DB 388 CGCTTCTCAGGAGTGTGATCTGGACAGACTTCACTCACCATTCTTACTGCTTCCAGCCT 447
QY 81 GlylnserProlyseuleuiletyrserAlaserAsnArgTyrthrclyValProap 100
DB 448 GAAAGCTTTCAGATTAATTAATGCTGACATTAATTAATTAATTAATTAATTAATTAAT 507
QY 101 GlythrclyleuqluileysargthrvAlaAlaProserValPheilepserProp 120
DB 508 GGGACCAAGGTGACATCAACAGACTGCTGACACTGCTTCTTACTTCTTCCGCCCA 567
QY 121 SeraspGluGlnleuyserserglythraAlaserValCysleuleuansanpheTyr 140
DB 568 TCTGATGACAGCTGTAATCTGGAACCTGCTCTGTTGTGTGCTGCTGATTAATCTTCT 627
QY 141 ProargGluAlaIyvalGlnTpyrValAspAsnAlaIleuGlnserGlyYansergln 160
DB 628 CCCAGAGAGGCCAAAGTACAGTGAAGGTGAATGAAGCCCTCCAAATCGGTTAACTCCCA 687
QY 161 GluserValThrclyGlnAspSerlyAspSerThrclySerleuserSerThrclyThr 180
DB 688 GAGAGTGTCAAGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 747
QY 181 LeuserLyAlaAspTyrGlnlyshIyValTyrAlaCysGlnuValThrclyGlnly 200
DB 748 CTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCCATCAGGGC 807
QY 201 LeuserSerProvalThrclySerPheAsnArgGlyGlyCys 214
DB 808 CTGAGCTCGCCGCTCAAAAGAGCTTCAACAGGAGAGAGTGT 849
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RESULT 5

US-10-714-000-16
; Sequence 16, Application US/10714000
; Publication No. US2005005310A1
; GENERAL INFORMATION:
; APPLICANT: Chisholm, Vanessa
; APPLICANT: Crowley, Craig W.
; APPLICANT: Krummen, Lynne A.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: EXPRESSION VECTORS AND METHODS
; FILE REFERENCE: P1746R1P1 US
; CURRENT APPLICATION NUMBER: US/10/714,000
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 10/019,586
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/18841
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/143,360
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 17

; SEQ ID NO 16
; LENGTH: 12514
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pSV.IPD.2C 4 circular ds-DNA
US-10-714-000-16

Alignment Scores:

Alignment Scores:
Pred. No.: 7.03e-110 Length: 12514
Score: 964.00 Matches: 185
Percent Similarity: 92.5% Conservative: 13
Best Local Similarity: 86.4% Mismatches: 16
Query Match: 86.4% Indels: 0
DB: 9 Gaps: 0

US-10-635-908-15 (1-214) x US-10-714-000-16 (1-12514)

```
QY 1 Aapllevalmetthrcinserglnargphmetserthrthrvaiqlvysparyvalser 20
DB 4211 GATATCCAGATGACCCAGTCCCTCCATCCCTGATCCATCAGATGAGAGACAGGCTCACC 4270
QY 21 IletthrcylvalaserglnasenvaiValserAlaValatPtyrtynglnlysp 40
DB 4271 ATCACCCTGCAAGCCAGTCAAGATGGGTGCTGCTGATGACTGCTATCAACAGAAACCA 4330
QY 41 GlylnserProlyseuleuiletyrserAlaserAsnArgTyrthrclyValProap 60
DB 4331 GAAAGCTTTCAGATTAATTAATGCTGACATTAATTAATTAATTAATTAATTAATTAAT 4390
QY 61 Argpethrclyserglyserglythraepthrclythraepthrclythraepthrcly 80
DB 4391 CGCTTCTCAGGAGTGTGATCTGGACAGACTTCACTCACCATCAACAGACTGAGTCCCTTCT 4450
QY 81 GlylnserProlyseuleuiletyrserAlaserAsnArgTyrthrclyValProap 100
DB 4451 GAAAGCTTTCAGATTAATTAATGCTGACATTAATTAATTAATTAATTAATTAATTAAT 4510
QY 101 GlythrclyleuqluileysargthrvAlaAlaProserValPheilepserProp 120
DB 4511 GGTACCAAGGTGAGATCAACAGACTGCTGACACTGCTTCTTACTTCTTCCGCCCA 4570
QY 121 SeraspGluGlnleuyserserglythraAlaserValCysleuleuansanpheTyr 140
DB 4571 TCTGATGACAGCTGTAATCTGGAACCTGCTCTGTTGTGTGCTGCTGATTAATCTTCT 4630
QY 141 ProargGluAlaIyvalGlnTpyrValAspAsnAlaIleuGlnserGlyYansergln 160
DB 4631 CCCAGAGAGGCCAAAGTACAGTGAAGGTGAATGAAGCCCTCCAAATCGGTTAACTCCCA 4690
QY 161 GluserValThrclyGlnAspSerlyAspSerThrclySerleuserSerThrclyThr 180
DB 4691 GAGAGTGTCAAGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 4750
QY 181 LeuserLyAlaAspTyrGlnlyshIyValTyrAlaCysGlnuValThrclyGlnly 200
DB 4751 CTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAAGTCAACCCATCAGGGC 4810
QY 201 LeuserSerProvalThrclySerPheAsnArgGlyGlyCys 214
DB 4811 CTGAGCTCGCCGCTCAAAAGAGCTTCAACAGGAGAGAGTGT 4852
```

RESULT 6

US-10-715-270-4
; Sequence 4, Application US/10715270
; Publication No. US20050019925A1
; GENERAL INFORMATION:
; APPLICANT: Krummen, Lynne A.
; APPLICANT: Shen, Amy Y.
; TITLE OF INVENTION: Intron Fusion Construct and Method of Using for
; FILE REFERENCE: P1937R1US
; CURRENT APPLICATION NUMBER: US/10/715,270

CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US 60/426,095
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 4
LENGTH: 12514
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: plasmid pSV.IPD.2C4 circular ds-DNA
NAME/KEY: Misc-feature
LOCATION: 444
OTHER INFORMATION: splice donor
FEATURE:
NAME/KEY: Misc-feature
LOCATION: 479
OTHER INFORMATION: start PUR coding
FEATURE:
NAME/KEY: Misc-feature
LOCATION: 1079-1643
OTHER INFORMATION: DHR coding region
FEATURE:
NAME/KEY: Misc-feature
LOCATION: 1883
OTHER INFORMATION: start 2C4 HC coding
FEATURE:
NAME/KEY: Misc-feature
LOCATION: 4154
OTHER INFORMATION: start LC coding
US-10-715-270-4

Alignment Scores:
Pred. No.: 7.03e-110 Length: 12514
Score: 964.00 Matches: 185
Percent Similarity: 92.5% Conservative: 13
Best Local Similarity: 86.4% Mismatches: 16
Query Match: 86.4% Indels: 0
DB: 9 Gaps: 0

US-10-635-908-15 (1-214) x US-10-715-270-4 (1-12514)
QY 1 AspIleValMetThrgInSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 4211 GAAATCCAGTATGACCCAGTCCCGAGCTCCCTGTCGCGCTCTGAGGCGATAGGATCACC 4270
QY 21 IleThrCylValAlaSerGlnAsnValValSerAlaValAlaTPrTyGlnGlnLysPro 40
DB 4271 ATCACCTGCAAGCCAGTCAAGATGCTCTATTGGTGTCTCCCTGGTATCAACAGAAACCA 4330
QY 41 GlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyThrgIValProAsp 60
DB 4331 GGAAGAGCTCGAAAGTACTGATTTACTCGGCTTCTTACCGATACATCGAGTCCCTTCT 4390
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 4391 CGCTTCTCGATCCGCTTCTGGGACGATTTCACTGACCAATCAGACATCTGACCA 4450
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleTySerAsnTyProTPrThrPheGlyGly 100
DB 4451 GAAGACTTCCCACTTATTACTGTCAACATATTATTATTCCTTACAGCTTGGACAG 4510
QY 101 GlyThrLysLeuGlnIleTySerGlyThrValAlaAlaProSerValPheIlePheProPro 120
DB 4511 GGTACCAAGGTGGAGATCAACAGACTGCTGCAATCTGCTTCACTTCCGCCCA 4570
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTy 140
DB 4571 TCTGATAGCAGTGTGAATCTGGAATCTGCTTGTGTGCTGCTGGAATTAATCTTAT 4630
QY 141 ProArgGlnAlaLysValGlnTPrLysValAlaAsnAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 4631 CCCAGAGAGGCCAAAGTACAGTGGAGGTGATTAACGCTTCAATCGGGTAACTCCAG 4690

QY 161 GluSerValThrGlnAlaAspSerLysAspSerThrTySerLeuSerSerThrLeuThr 180
DB 4691 GAGAGTGTCAACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 4750
QY 181 LeuSerLysAlaAspTyGlnLysHisLysValTyrAlaCysGlnValThrIleGlnGly 200
DB 4751 CTGAGCAAGACAGACTACAGAAACACAAAGTCTACGCTTGGGAATCAACCATCAGGGC 4810
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlnCys 214
DB 4811 CTGAGCTGCCCGCTCAACAAAGAGCTTCAACAGGAGAGAGTGT 4852

RESULT 7

US-10-377-121-15
Sequence 15, Application US/10377121
Publication No. US20040001825A1
GENERAL INFORMATION:
APPLICANT: GOVINDAM, SERENGULAM
APPLICANT: QU, ZHENGXING
APPLICANT: HANSEN, HANS
APPLICANT: GOLDENBERG, DAVID
TITLE OF INVENTION: RS7 ANTIBODIES
FILE REFERENCE: 018733/1163
CURRENT APPLICATION NUMBER: US/10/377,121
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 60/360,299
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 702
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(699)
US-10-377-121-15

Alignment Scores:
Pred. No.: 1.17e-110 Length: 702
Score: 956.00 Matches: 185
Percent Similarity: 92.5% Conservative: 13
Best Local Similarity: 86.4% Mismatches: 16
Query Match: 85.7% Indels: 0
DB: 7 Gaps: 0

US-10-635-908-15 (1-214) x US-10-377-121-15 (1-702)
QY 1 AspIleValMetThrgInSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 58 GACATCCAGTCAAGCCAGTCTCCATCTCCCTGCTGCACTGTAGAGACAGAGTACG 117
QY 21 IleThrCylValAlaSerGlnAsnValValSerAlaValAlaTPrTyGlnGlnLysPro 40
DB 118 ATCACCTGCAAGCCAGTCAAGATGATGATTTGCTTACCTGATACAGACAAACCA 177
QY 41 GlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyThrgIValProAsp 60
DB 178 GGAAGAGCTCGAAAGTACTGATTTACTCGGCTTCTTACCGATACATCGAGTCCCTGAT 237
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 238 AGGTTCAGTGCAGTGGATCTGGAGACGATTTCACTTCAACATCAGACAGCTGCAACT 297
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnIleTySerAsnTyProTPrThrPheGlyGly 100
DB 298 GAGATTTTTCAGTTTATTACTGTCAACATATTATTACTCGCTCACAGTTCGCTGCT 357
QY 101 GlyThrLysLeuGlnIleTySerGlyThrValAlaAlaProSerValPheIlePheProPro 120
DB 358 GGGACCAAGGTGGAGATCAACAGTACTGTGCTGCAACATCTGCTTCACTTCCGCCCA 417

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QY 121 SerApgGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPhetYr 140
Db 418 TCTGATGAGCAATTGAAATCTGGAACCTGCTCTGTTGTGTGCTGCTGAAATTAATCTTAT 477
QY 141 ProApgGluAlaLysValGlnTrpLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 478 CCCAAGAGAGGCCAAAGTACAGTGAAGGTGATTAACGCTCTCAATCGGGTAATCTCCAG 537
QY 161 GluSerValThrGluGlnAspSerLysAspSerThrTrpSerLeuSerSerThrLeuThr 180
Db 538 GAGATGTCACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 597
QY 181 LeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200
Db 598 CTGACCAAGCAGACTACAGCAAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGCG 657
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
Db 658 CTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 699

RESULT 8
US-10-377-121-19
; Sequence 19, Application US/10377121
; Publication No. US20040001825A1
; GENERAL INFORMATION:
; APPLICANT: GOVINDAM, SERENGULAM
; APPLICANT: OU, ZHENGXING
; APPLICANT: HANSEN, HANS
; APPLICANT: GOLDENBERG, DAVID
; TITLE OF INVENTION: RS7 ANTIBODIES
; FILE REFERENCE: 018733/1163
; CURRENT APPLICATION NUMBER: US/10/377,121
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/360,299
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(699)
US-10-377-121-19

Alignment Scores:
Pred. No.: 1,176-110 Length: 702
Score: 956.00 Matches: 185
Percent Similarity: 92.5% Conservative: 13
Best Local Similarity: 86.4% Mismatches: 16
Query Match: 85.7% Indels: 0
DB: 7 Gaps: 0

US-10-635-908-15 (1-214) x US-10-377-121-19 (1-702)
QY 1 AspLeValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 58 GACATCCAGCTGACCCAGTCTCCATCTCCTCTGCGCATCTTACCGGATCACTGAGATCCCTGAT 117
QY 21 IleThrCysLysValAspSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
Db 118 ATCACCTGCAAGGCCAGATCAGATGTGATGATTGCTGTACCTCGGATTCAGCAGAAACCA 177
QY 41 GlyGlnSerProLysLeuLeuLysIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db 178 GGGAAAGCCCTTAAGCTCTGATCTTACTCGGCATCTTACCGGATCACTGAGATCCCTGAT 237
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 238 AGGTTCAAGTGGAGTGAATCTGGGACAGATTTCACCTCTACCAATCAGACAGTCTGCAACT 297
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
```

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Db 298 GAAAGATTTTGGCAATTATTACTGTCAGCAACATTTATATTACTCCGCTCAGCTTCAGTGT 357
QY 101 GlyThrLysLeuGluLysValGlnThrValAlaAlaProSerValPheIlePheProPro 120
Db 358 GGGACCAAGCTGAGATTAAGCTACTGTGGTGCACCATCTGTCTTACTTCTCCGCCCA 417
QY 121 SerApgGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPhetYr 140
Db 418 TCTGATGAGCAATTGAAATCTGGAACCTGCTCTGTTGTGTGCTGCTGAAATTAATCTTAT 477
QY 141 ProApgGluAlaLysValGlnTrpLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 478 CCCAAGAGAGGCCAAAGTACAGTGAAGGTGATTAACGCTCTCAATCGGGTAATCTCCAG 537
QY 161 GluSerValThrGluGlnAspSerLysAspSerThrTrpSerLeuSerSerThrLeuThr 180
Db 538 GAGATGTCACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 597
QY 181 LeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGly 200
Db 598 CTGACCAAGCAGACTACAGCAAGAAACAAAGTCTACGCTGCGAAGTCAACCATCAGGCG 657
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGluCys 214
Db 658 CTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 699

RESULT 9
US-10-281-479A-55
; Sequence 55, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: Lobuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THE
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.002906
; CURRENT APPLICATION NUMBER: US/10/281,479A
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 711
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synth
US-10-281-479A-55

Alignment Scores:
Pred. No.: 1,846-110 Length: 711
Score: 954.50 Matches: 185
Percent Similarity: 93.5% Conservative: 15
Best Local Similarity: 86.4% Mismatches: 13
Query Match: 85.5% Indels: 1
DB: 7 Gaps: 1

US-10-635-908-15 (1-214) x US-10-281-479A-55 (1-711)
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```

QY 1 AaplleValMeThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 61 GACATTGTGATGACCCCAATCTCCAAAGTCTTTGTCTGCACTCTGTGGGACAGGGTCCAC 120
QY 21 ILeThrCysLysAlaSerGlnAenValIvalSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 121 ATCACCTGCAGAGCCAGTCAGATGTGGGTACTGCTGTAGCCCTGTATCAACAGAAACCA 180
QY 41 GlyGlnSerProLysLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 181 GGGAAAGCTCCTTAACCTACTGATTTACTGGGCATCCACCGACACTGGGGTCCCAAGC 240
QY 61 ArgPheThrGlySerGlySerGlyTyrThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 241 AGGTTAGTGGAGCTGGGTCTGGGACAGACTTCACTCCATCTCTACTGTGCAAGCCG 300
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
DB 301 GAGGATTTTGCACCTATTACTGTCAAGCATATAGTATATCGG--ACGTTCCGGTCAA 357
QY 101 GlyThyLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 358 GGCACCAAGGTGGAATCAAAACGAGCTGTGGCTGCACCATCTGTTCATCTTCCGCCA 417
QY 121 SerAspGlnGlnLeuLysSerGlyTyrThrAlaSerValValCysLeuLeuAenAsnPheTyr 140
DB 418 TCTGATGAGCAGTTGAATCTGGAATCTGCTCTGTGTGTGTGCTGTGAATTAATTCTAT 477
QY 141 ProArgGlnAlaLysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 478 CCCAGAGAGGCCAAAGTACAGTGGAGAGTGATTAACCCCTCCAAATGGGTAACTCCAG 537
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 538 GAGGTGTCTCAGAGCAGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 597
QY 181 LeuSerLysAlaAspTyrGlnLysLysLysValTyrAlaCysGluValThrHisGlnGly 200
DB 598 CTGAGCAAGCAGACTCTCGAGAAACAAAGTCTACGCTCGCAAGTCAACCCATCAGAGGC 657
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB 658 CTGAGCTCGCCCGTCAACAAGAGCTTCAACAGGGGAGAGTGT 699

RESULT 10
US-10-275-180A-55
; Sequence 55, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002905
; CURRENT APPLICATION NUMBER: US/10/275.180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./No. US20030190687A1e =
US-10-275-180A-55

Alignment Scores: 1.84e-110 Length: 711

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Score: 954.50 Matches: 185
Percent Similarity: 93.5% Conservative: 15
Best Local Similarity: 86.4% Mismatches: 13
Query Match: 85.5% Indels: 1
DB: 7 Gaps: 1

US-10-635-908-15 (1-214) x US-10-275-180A-55 (1-711)

QY 1 AaplleValMeThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 61 GACATTGTGATGACCCCAATCTCCAAAGTCTTTGTCTGCACTCTGTGGGACAGGGTCCAC 120
QY 21 ILeThrCysLysAlaSerGlnAenValIvalSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 121 ATCACCTGCAGAGCCAGTCAGATGTGGGTACTGCTGTAGCCCTGTATCAACAGAAACCA 180
QY 41 GlyGlnSerProLysLeuLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 181 GGGAAAGCTCCTTAACCTACTGATTTACTGGGCATCCACCGACACTGGGGTCCCAAGC 240
QY 61 ArgPheThrGlySerGlySerGlyTyrThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 241 AGGTTAGTGGAGCTGGGTCTGGGACAGACTTCACTCCATCTCTACTGTGCAAGCCG 300
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
DB 301 GAGGATTTTGCACCTATTACTGTCAAGCATATAGTATATCGG--ACGTTCCGGTCAA 357
QY 101 GlyThyLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 358 GGCACCAAGGTGGAATCAAAACGAGCTGTGGCTGCACCATCTGTCTTCACTTCCGCCA 417
QY 121 SerAspGlnGlnLeuLysSerGlyTyrThrAlaSerValValCysLeuLeuAenAsnPheTyr 140
DB 418 TCTGATGAGCAGTTGAATCTGGAATCTGCTCTGTGTGTGTGCTGTGAATTAATTCTAT 477
QY 141 ProArgGlnAlaLysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 478 CCCAGAGAGGCCAAAGTACAGTGGAGAGTGATTAACCCCTCCAAATGGGTAACTCCAG 537
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 538 GAGGTGTCTCAGAGCAGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 597
QY 181 LeuSerLysAlaAspTyrGlnLysLysLysValTyrAlaCysGluValThrHisGlnGly 200
DB 598 CTGAGCAAGCAGACTCTCGAGAAACAAAGTCTACGCTCGCAAGTCAACCCATCAGAGGC 657
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB 658 CTGAGCTCGCCCGTCAACAAGAGCTTCAACAGGGGAGAGTGT 699

RESULT 11
US-10-286-132A-55
; Sequence 55, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Lobuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002907
; CURRENT APPLICATION NUMBER: US/10/286.132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02

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/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 55
/ LENGTH: 711
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence://No. US20030198637A1e = Synthe
US-10-286-132A-55

Alignment Scores:
Pred. No.: 1,84e-110 Length: 711
Score: 954.50 Matches: 165
Percent Similarity: 93.5% Conservative: 15
Best Local Similarity: 86.4% Mismatches: 13
Query Match: 85.5% Indels: 1
DB: Gaps: 1

US-10-635-908-15 (1-214) x US-10-286-132A-55 (1-711)

QY 1 AapllevalmetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
Db 61 GACATTGTATGACCCCAATCTCCAAAGTCTTGTCTGCACTCTGGGGGACAGGGGTCCACC 120
QY 21 IletHrCyAlaValAspSerGlnAsnValValSerAlaValAlaTyrPyrGlnGlnIlyPro 40
Db 121 ATCACTTGCAAGGCGCATGCAAGATGGGATCTGCTGATGCTGATCAACAGAAACCA 180
QY 41 GlyGlnSerProIlyLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db 181 GGGAAAGCTCTTAATCTAGATTTTACTGGGACATCCAGCGGACACTGGGGTCCCAAGC 240
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 241 AGGTTTACGGGAGTGGTGTCTGGACAGACTTCACCTCACTCTGTGTGTCAGCGCCG 300
QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTyrPheGlyGly 100
Db 301 GAGGATTTTGCACCTATTACTGTACGACATATAGTATTCGG--ACGTTCCGATCA 357
QY 101 GlyThrIlyLeuGlnIleIlyAsArgThrValAlaAlaProSerValPheIlePhePro 120
Db 358 GGCACCAAGGTGAAATCAACCGACTGTGGTGCACCATCTGTCTTCACTTCCGCCCA 417
QY 121 SerAspGlnGlnLeuIlySerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db 418 TCTGATGACAGAGTGGAAATCTGGAACTGCTCTGTGTGTGCTGTGATTAATCTTCTAT 477
QY 141 ProArgGluAlaIlyValGlnTyrIlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 478 CCCAGAGAGGCCAAAGTACGTGAAAGTGGATTAAGCCCTCCAAATCGGGTAACTCCAG 537
QY 161 GluSerValThrGlnGlnAspSerIlyAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 538 GAGAGTGTCAACAGACGAGCAGCAAGACAGACACCTACAGCCTCAGCAGCAGCCTGAGC 597
QY 181 LeuSerIlyAlaAspTyrGlnIlyIlyValIlyValIlyValIlyValIlyValIlyVal 200
Db 598 CTGAGCAAAAGCACTACGAGAAACCAAAAGTCTACGCCCTGCGAAAGTCAACCATCAGGGC 657
QY 201 LeuSerSerProValThrIlySerPheAsnArgGlyGluCys 214
Db 658 CTGAGCTCGCCCTTCAACAAAGAGCTTCAACAGGGGAGAGTGT 699

RESULT 12
US-09-949-559-127
/ Sequence 127, Application US/09949559
/ Patent No. US20020151682A1
/ GENERAL INFORMATION:
/ APPLICANT: Achwal, Diljeet Singh
/ APPLICANT: Brown, Derek Thomas
/ APPLICANT: Weir, Andrew Neil Charles
/ APPLICANT: Popplewell, Andrew George
```

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/ APPLICANT: Chapman, Andrew Paul
/ APPLICANT: King, David John
/ TITLE OF INVENTION: Biological Products
/ FILE REFERENCE: Carp-0095
/ CURRENT APPLICATION NUMBER: US/09/949,559
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 0013810.7GB
/ PRIOR FILING DATE: 2000-06-06
/ PRIOR APPLICATION NUMBER: 09/875,221
/ NUMBER OF SEQ ID NOS: 130
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 127
/ LENGTH: 642
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Grafted light chain for fab and modified fab
US-09-949-559-127

Alignment Scores:
Pred. No.: 1,06e-109 Length: 642
Score: 948.00 Matches: 183
Percent Similarity: 92.1% Conservative: 14
Best Local Similarity: 85.5% Mismatches: 17
Query Match: 84.9% Indels: 0
DB: Gaps: 0

US-10-635-908-15 (1-214) x US-09-949-559-127 (1-642)

QY 1 AapllevalmetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
Db 1 GACATTCAATATACCAAGCCCATCCAGCCCTCGAGGCGATCTGTAGAGACCGGGTCCACC 60
QY 21 IletHrCyAlaValAspSerGlnAsnValValSerAlaValAlaTyrPyrGlnGlnIlyPro 40
Db 61 ATCACTTGAAAGCCAGTACAGAACGATAGTACTTAAGTACGCTGTATACGCAAAAACCA 120
QY 41 GlyGlnSerProIlyLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
Db 121 GGTAAAGCCCAAGCCCTCATCTACAGTGCCTCTTCTCTATAGTGTGTACCATAC 180
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
Db 181 AGCTTACGGGATCCGATGTGTGATCTTACACCTACACATCAGTACGCTCCAGCCA 240
QY 81 GluAspLeuAlaAspPheCysGlnGlnTyrSerAsnTyrProTyrPheGlyGly 100
Db 241 GAAAGATTTGCCCATATTACTGTCAACAGTATTAATCATCTACCATTCACATTCCGTGAC 300
QY 101 GlyThrIlyLeuGlnIleIlyAsArgThrValAlaAlaProSerValPheIlePhePro 120
Db 301 GGTACTAAAGTGAATCAACGTACGTAGCGGCCCATCTGTCTTCACTTCCGCCCA 360
QY 121 SerAspGlnGlnLeuIlySerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
Db 361 TCTGATGACAGATGAAATCTGAACTGCTCTGTGTGTGCTGTGATTAATCTTCTAT 420
QY 141 ProArgGluAlaIlyValGlnTyrIlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
Db 421 CCCAGAGAGGCCAAAGTACGTGAAAGTGGATTAAGCCCTCCAAATCGGGTAACTCCAG 480
QY 161 GluSerValThrGlnGlnAspSerIlyAspSerThrTyrSerLeuSerSerThrLeuThr 180
Db 481 GAGAGTGTCAACAGACGAGCAGCAAGACAGACCTACAGCCTCAGCAGCAGCCTGAGC 540
QY 181 LeuSerIlyAlaAspTyrGlnIlyIlyValIlyValIlyValIlyValIlyValIlyVal 200
Db 541 CTGAGCAAAAGCACTACGAGAAACCAAAAGTCTACGCCCTGCGAAAGTCAACCATCAGGGC 600
QY 201 LeuSerSerProValThrIlySerPheAsnArgGlyGluCys 214
Db 601 CTGAGCTCACAGTAAACAAAGCTTAAATAGAGAGAGTGT 642
```


RESULT 13

US-09-875-221A-127
Sequence 127, Application US/09875221A
Publication No. US2003026805A1
GENERAL INFORMATION:
APPLICANT: Achwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0089
CURRENT APPLICATION NUMBER: US/09/875,221A
CURRENT FILING DATE: 2001-06-06
PRIORITY FILING DATE: 2000-06-06
PRIORITY FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 127
LENGTH: 642
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Grafted light chain for fab and modified fab
US-09-875-221A-127

Alignment Scores:

Pred. No.:	1,06e-109	Length:	642
Score:	948.00	Matches:	183
Percent Similarity:	92.1%	Conservative:	14
Best Local Similarity:	85.5%	Mismatches:	17
Query Match:	84.9%	Indels:	0
DB:	3	Gaps:	0

US-10-635-908-15 (1-214) x US-09-875-221A-127 (1-642)

```
QY 1 AsplleValMetThrgInserGlnArgPheMetSerThrValGlyAspArgValSer 20
DB 1 GACATTGAAATGAGCCAGAGCCATCCAGCTGAGCCGATGTGAGAGACCGGATCAC 60
QY 21 IleThrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 61 ATCTCTGTAAAGCCAGTCAAGAGTACGTACTTAAGCTGTATCGCAAAAACCA 120
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 121 GGTAAAGCCCAAAAGCCCTCATCTACAGTCCCTCTTCTCTATGAGGTGTACCATAC 180
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 181 AGGTTCAGCCGATCCGATGAGTGTGATTTCAACCTCAGATCAGATGAGCTCAGCCA 240
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly 100
DB 241 GAAGTTTCGCCACTATTTACTGTCAACAGTAACATCTACCACTCAGATTCGGTACG 300
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 301 GGTACTAAAGTAAATCAATCAACGTAACGATACCGGCCCATCTGCTTCATCTCCGCA 360
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 361 TCTGATGAGAGTGAATCTGAACTCTCTGTGTGTGCTGCTCTCAATTAATCTTCTAT 420
QY 141 ProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 421 CCCAGAGAGGCCAAAGTAACTAGTGAAGGTGATACCGCTCCATCGGTAATCTCCAG 480
QY 161 GluSerValThrGlnGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 481 GAGAGTGTACAGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 540
```

RESULT 14

US-10-310-454-3
Sequence 3, Application US/10310454
Publication No. US20030157061A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
TITLE OF INVENTION: Combinations of a Cyclooxygenase-2 Selective Inhibitor and a TNF
FILE REFERENCE: 18438/09008
CURRENT APPLICATION NUMBER: US/10/310,454
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 642
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Grafted Light Chain for Fab and Modified Fab
NAME/KEY: CDS
LOCATION: (1)..(642)
OTHER INFORMATION:
US-10-310-454-3

Alignment Scores:

Pred. No.:	1,06e-109	Length:	642
Score:	948.00	Matches:	183
Percent Similarity:	92.1%	Conservative:	14
Best Local Similarity:	85.5%	Mismatches:	17
Query Match:	84.9%	Indels:	0
DB:	7	Gaps:	0

US-10-635-908-15 (1-214) x US-10-310-454-3 (1-642)

```
QY 1 AsplleValMetThrgInserGlnArgPheMetSerThrValGlyAspArgValSer 20
DB 1 GACATTGAAATGAGCCAGAGCCATCCAGCTGAGCCGATGTGAGAGACCGGATCAC 60
QY 21 IleThrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrGlnGlnLysPro 40
DB 61 ATCTCTGTAAAGCCAGTCAAGAGTACGTACTTAAGCTGTATCGCAAAAACCA 120
QY 41 GlyGlnSerProLysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValProAsp 60
DB 121 GGTAAAGCCCAAAAGCCCTCATCTACAGTCCCTCTTCTCTATGAGGTGTACCATAC 180
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnMetGlnSer 80
DB 181 AGGTTCAGCCGATCCGATGAGTGTGATTTCAACCTCAGATCAGATGAGCTCAGCCA 240
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTyrThrPheGlyGly 100
DB 241 GAAGTTTCGCCACTATTTACTGTCAACAGTAACATCTACCACTCAGATTCGGTACG 300
QY 101 GlyThrLysLeuGlnIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120
DB 301 GGTACTAAAGTAAATCAATCAACGTAACGATACCGGCCCATCTGCTTCATCTCCGCA 360
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyr 140
DB 361 TCTGATGAGAGTGAATCTGAACTCTCTGTGTGTGCTGCTCTCAATTAATCTTCTAT 420
QY 141 ProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
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Db 421 CCCAGAGAGCCCAAGTACAGTGGAGAGTGGATACGCCCTCCATCGGCTACTCCAG 480
Qy 161 GluSerValThrGluGlnAAspSerIlyAspSerThrIYSerIeuSerSerThrIeuThr 180
Db 481 GAGAGTGTACACAGAGCAGAGCAGACAGACAGACCTACAGCTCAGCAGACCTGAGC 540
Qy 181 IeuSerIlyAlaAspIlyGluIlyshIlyValIYAlaCyGluValThrIseGIngly 200
Db 541 CTGAGCAAGCAGACTACAGAAACAAAGTCTAGCCTGCGAAGTCAACCATCAGGAG 600
Qy 201 IeuSerSerProValThrIlySerPheAsnArgGlyGlyCys 214
Db 601 CTGAGCTCACCACTAACAAAGCTTTATAGAGGAGAGTGT 642

RESULT 15
US-10-401-344-3
; Sequence 3, Application US/10401344
; Publication No. US20030194404A1
; GENERAL INFORMATION:
; APPLICANT: Schering Corporation and Abgenix, Inc.
; APPLICANT: Greenfeder, Scott
; APPLICANT: Corvalan, Jose
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COME
; TITLE OF INVENTION: COMPRISING SAME
; FILE REFERENCE: LI01564W1
; CURRENT APPLICATION NUMBER: US/10/401,344
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-401-344-3
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Alignment Scores:
pred. No.: 2,94e-109 length: 708
Score: 945.00 Matches: 178
Percent Similarity: 92.5% Conservative: 20
Best Local Similarity: 83.2% Mismatches: 16
Query Match: 84.7% Indels: 0
DB: 7 Gaps: 0
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US-10-635-908-15 (1-214) X US-10-401-344-3 (1-708)

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Qy 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
Db 67 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCGATCTGTGGAGACAGAGTCACG 126
Qy 21 IleThrCylValAlaSerGlnAsnValValSerIleValAlaTrpIlyGlnGlnIlyPro 40
Db 127 ATCACTTGCCAGCGGAGTCAAGACATTAATTAATTAATTAATTAATTAATTAATTAAT 186
Qy 41 GlyIleSerProIlyIeuIeuIleIYSerAlaSerAsnArgIYThrGlyValProAsp 60
Db 187 GGGAAAGCCCTTAACCTCCGATCTACAGTCTTCCATTGGAAACAAAGATCCCATCA 246
Qy 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIeuThrIleSerAsnMetGlnSer 80
Db 247 AGGTTGAGTGAAGTGTCTTGGGACAGATTTTACTTTCACCATCAGACGCTGACAGCT 306
Qy 81 GluAspIleuAlaAspPhePheCyGlnGlnIlySerAsnIYProTrpThrPheGlyGly 100
Db 307 GAAGATATGTGCAACATATTTGTCAACAGTATGATATATACCCGCTCACTTCGGGGGA 366
Qy 101 GlyThrIlyIeuGlnIlyIleYArgThrValAlaIleProSerValPheIlePheProPro 120
Db 367 GGGACCAAGGTGAGATCAACAGACTGTGCTGCACCATCTGTCTTCACTTCCCGCCA 426
Qy 121 SerAspGlnIleuIlySerGlyThrAlaSerValValCysIleuIeuAsnAsnIly 140
Db 427 TCTGATGAGCAGTGAATCTGGAATGCTGCTGTTGTGTGCTGTAATTAACCTTCTAT 486
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Qy 141 ProArgGluAlaIlyValGlnTrpIlyValIleuGlnSerGlyAsnSerGln 160
Db 487 CCCAGAGAGCCCAAGTACAGTGAAGGTGAACGCCCTCCATCGGCTACTCCAG 546
Qy 161 GluSerValThrGluGlnAAspSerIlyAspSerThrIYSerIeuSerSerThrIeuThr 180
Db 547 GAGAGTGTACACAGAGCAGAGCAGACAGACAGACCTACAGCTCAGCAGACCTGAGC 606
Qy 181 IeuSerIlyAlaAspIlyGluIlyshIlyValIYAlaCyGluValThrIseGIngly 200
Db 607 CTGAGCAAGCAGACTACAGAAACAAAGTCTAGCCTGCGAAGTCAACCATCAGGAG 666
Qy 201 IeuSerSerProValThrIlySerPheAsnArgGlyGlyCys 214
Db 667 CTGAGCTCACCACTAACAAAGCTTTATAGAGGAGAGTGT 708
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Search completed: June 3, 2006, 07:32:32
Job time : 1481.01 secs

Tue Jun 6 10:54:29 2006

us-10-635-908-15.rmpbn

GenCore version 5.1.9
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OW protein - nucleic search, using frame_plus_p2n model

Run on: June 3, 2006, 06:56:49 ; Search time 24.4204 Seconds
(Without alignments)
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Title: US-10-635-908-15
Sequence: 1 D1VMTQSQRFMTSTVGDVRS.....EVTHQGLSSPVTKSFNRGEC 214

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 246837 segs, 5886590 residues
Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=abs/ABSSWB.spool/US10635908/runat_02062006_104226_10433/app_query.fasta.1
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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsun62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
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2: /EMC_Celerra_SIDS3/prodata/2/pubpna/US06_NEW_PUB.seq:
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7: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11_NEW_PUB.seq:
8: /EMC_Celerra_SIDS3/prodata/2/pubpna/US60_NEW_PUB.seq:
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1007	90.2	1701	7	US-11-106-762-10 Sequence 10, Appl
2	964	86.4	862	7	US-11-219-563-129 Sequence 129, Appl
3	937	84.0	642	6	US-10-981-300-17 Sequence 17, Appl
4	936	83.9	705	7	US-11-211-917-23 Sequence 23, Appl
5	934	83.7	705	6	US-10-546-594-131 Sequence 131, Appl
6	933	83.6	642	6	US-10-981-300-13 Sequence 13, Appl
7	929	83.2	645	7	US-11-155-444-3 Sequence 3, Appl
8	928	83.2	705	7	US-11-211-917-47 Sequence 47, Appl
9	901	80.7	705	7	US-11-211-917-87 Sequence 87, Appl

10	900	80.6	645	7	US-11-155-444-19	Sequence 19, Appl
11	878	78.7	705	7	US-11-211-917-71	Sequence 71, Appl
12	872.5	78.2	720	7	US-11-211-917-39	Sequence 39, Appl
13	869.5	77.9	720	7	US-11-211-917-31	Sequence 31, Appl
14	868	77.8	929	7	US-11-293-697-1838	Sequence 1838, Ap
15	867.5	77.7	720	7	US-11-211-917-15	Sequence 15, Appl
16	867.5	77.7	720	7	US-11-211-917-101	Sequence 101, App
17	867.5	77.7	9209	7	US-11-183-218-58	Sequence 58, Appl
18	865.5	77.6	720	7	US-11-211-917-7	Sequence 7, Appl1
19	865.5	77.6	720	7	US-11-211-917-85	Sequence 55, Appl
20	865.5	77.6	944	7	US-11-293-697-1585	Sequence 1585, Ap
21	864.5	77.5	720	7	US-11-211-917-79	Sequence 79, Appl
22	863.5	77.4	720	7	US-11-211-917-63	Sequence 63, Appl
23	843	75.5	9780	7	US-11-187-863-1	Sequence 1, Appl1
24	808.5	72.4	9400	7	US-11-297-317-17	Sequence 17, Appl
25	785.5	70.4	9362	7	US-11-297-317-18	Sequence 18, Appl
26	689.5	61.8	654	6	US-10-506-063A-11	Sequence 11, Appl
27	644.5	57.8	626	6	US-10-506-063A-19	Sequence 19, Appl
28	639	57.3	1810	7	US-11-293-697-1650	Sequence 1650, Ap
29	625	56.0	494	1	US-09-784-950-80	Sequence 80, Appl
30	624	55.9	514	6	US-10-981-300-9	Sequence 9, Appl1
31	612	54.8	465	6	US-10-981-300-1	Sequence 1, Appl1
32	599	53.7	463	6	US-10-981-300-5	Sequence 5, Appl1
33	584.5	52.1	8540	7	US-11-183-218-57	Sequence 57, Appl
34	559	50.4	441	1	US-09-784-950-73	Sequence 73, Appl
35	556	49.8	441	1	US-09-784-950-69	Sequence 69, Appl
36	553	49.6	334	7	US-11-219-563-133	Sequence 133, App
37	531	47.6	441	1	US-09-784-950-65	Sequence 65, Appl
38	528	47.3	447	1	US-09-784-950-67	Sequence 67, Appl
39	502.5	45.0	445	1	US-09-784-950-75	Sequence 75, Appl
40	492.5	44.1	431	1	US-09-784-950-71	Sequence 71, Appl
41	484.5	43.4	444	1	US-09-784-950-63	Sequence 63, Appl
42	482.5	43.2	2196	7	US-11-155-444-5	Sequence 5, Appl1
43	482.5	43.2	2208	7	US-11-155-444-9	Sequence 9, Appl1
44	472	42.3	756	7	US-11-330-353-17	Sequence 17, Appl
45	466	41.8	375	6	US-10-546-594-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-11-106-762-10
; Sequence 10, Application US/11106762
; Publication No. US20060099662A1
; GENERAL INFORMATION:
; APPLICANT: CHUNTHARAPAI, ANAN ET AL.
; TITLE OF INVENTION: ASSAY FOR ANTIBODIES
; FILE REFERENCE: P2075R1
; CURRENT APPLICATION NUMBER: US/11/106,762
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,193
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 10
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 1684
; OTHER INFORMATION: Unknown amino acid
US-11-106-762-10

Alignment Scores:

Pred. No.: 8.66e-94
Score: 1007.00
Percent Similarity: 95.3%
Best Local Similarity: 90.2%
Query Match: 90.2%
DB: 7
US-10-635-908-15 (1-214) x US-11-106-762-10 (1-1701)

Length: 1701
Matches: 193
Conservative: 11
Mismatch: 10
Indels: 0
Gaps: 0

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QY 1 AapllevalmetThGlnserGlnargPheMetSerThrValGlyAspArgValSer 20
DB 109 GATATCGTATGATACCCAGTCTCAAGATTCATGTCACATCGTAGAAGACAGGGTCACG 168
QY 21 IletnCyAlaValAlaSerGlnAnValAlaSerAlaValAlaTPTyrGlnGlnLysPro 40
DB 169 GTACCTGACAGAGCCGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 228
QY 41 GlnInserProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 229 GGGCAATCTCTTAAACCACTGATTTACTCGGCACTCTTACCGGAGTGTGGGCTCTGAT 288
QY 61 ArgPheThrGlySerGlySerGlyThrArgPheThrLeuThrIleSerAnMetGlnSer 80
DB 289 CGCTTCACAGGACGATGATCTCGACAGATTCATCTCACTCACTCACTCACTCACTCACTCACT 348
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
DB 349 GAAAGACTTGGCAGAGATCTTCTGTCAAGCATATCACAGTTTCCGTGAGAGTTCCGCTGGA 408
QY 101 GlyThrLysLeuGlnLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
DB 409 GGATCCAAAGGTGAGATCAAAACCACTGTGCTGACCACTCTCTTCACTCTTCCCGCCA 468
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValCysLeuLeuAnsnPheTyr 140
DB 469 TCTGATGAGCAGTTGAAATCTGAACTGCTTCTGTGTGTGCTGCTGCTGCTGCTGCTGCT 528
QY 141 ProArgGlnAlaLysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAnsnSerGln 160
DB 529 CCCAGAGAGCCAAAGTACGCTGGAAGTGTGATTAAGCCCTCCAACTCGGTTACTCCGAG 588
QY 161 GluSerValThrGlnLysAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 589 GAGAGTGTCAAGAGCAGACAGCAACCAAGACCACTACAGCCTCAGACAGCAGCCTGAGCG 648
QY 181 LeuSerLysAlaAspTyrGlyLysLysValTyrAlaCysGlnValThrHisGlnGly 200
DB 649 CTGAGCAAGACAGCTACGAGAAACAAAGTCTACGCTGCGAGTCAAGTCAAGTCAAGGCG 708
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB 709 CTGAGCTCGCCCTCAACAAAGACTTCAACAGGAGAGTGT 750

RESULT 2
US-11-219-563-129
; Sequence 129, Application US/11219563
; Publication No. US2006088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MEMBRANE ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 862
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain variable and constant region of ded591
; NAME/KEY: CDS
; LOCATION: (151) ... (849)
; US-11-219-563-129
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Alignment Scores:
Pred. No.: 8,826-90 Length: 862
Score: 964.00 Matches: 183
Percent Similarity: 93.5% Conservative: 17
Best Local Similarity: 85.5% Mismatches: 14
Query Match: 86.4% Indels: 0
DB: 7 Gaps: 0

US-10-635-908-15 (1-214) x US-11-219-563-129 (1-862)
QY 1 AapllevalmetThGlnserGlnargPheMetSerThrValGlyAspArgValSer 20
DB 208 GATATCGTATGATACCCAGTCTCAAGATTCATGTCACATCGTAGAAGACAGGGTCACG 267
QY 21 IletnCyAlaValAlaSerGlnAnValAlaSerAlaValAlaTPTyrGlnGlnLysPro 40
DB 268 CTCACCTGTAAGCCAGTCAAGATGTGGTACTGCTGTGAGACTGGTATCAAGAAACCA 327
QY 41 GlnInserProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 328 GGAACATCTCTTAACTACTGATTTATTTGGGATCTCACTGGACACTTCAAGCAATTCCTTA 387
QY 61 ArgPheThrGlySerGlySerGlyThrArgPheThrLeuThrIleSerAnMetGlnSer 80
DB 388 CGCTTCACAGGACGATGATCTGGAAGACTTCACTCACTCACTCACTCACTCACTCACTCACT 447
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTyrSerAsnTyrProTrpThrPheGlyGly 100
DB 448 GAAAGACTTGGCAGAGATCTGGAAGTGTGATTAAGCCCTCCAACTCGGTTACTCCGAG 507
QY 101 GlyThrLysLeuGlnLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
DB 508 GGAACCAAGTGTGACCTCAAGCAAGTGTGCTGACCACTGTCTTCACTTCCCGCCA 567
QY 121 SerAspGlnGlnLeuLysSerGlyThrAlaSerValCysLeuLeuAnsnPheTyr 140
DB 568 TCTGATGAGCAGTTGAAATCTGAACTGCTTCTGTGTGTGCTGCTGCTGCTGCTGCTGCT 627
QY 141 ProArgGlnAlaLysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAnsnSerGln 160
DB 628 CCAGAGAGAGCCAAAGTACAGTGAAGTGTGATTAAGCCCTCCAACTCGGTTACTCCGAG 687
QY 161 GluSerValThrGlnLysAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThr 180
DB 688 GAGAGTGTCAAGAGCAGACAGCAAGCAAGCTACAGCCTCAGCAGCAGCCTGAGCG 747
QY 181 LeuSerLysAlaAspTyrGlyLysLysValTyrAlaCysGlnValThrHisGlnGly 200
DB 748 CTGAGCAAGACAGCTACGAGAAACAAAGTCTACGCTGCGAAGTCAAGTCAAGTCAAGGCG 807
QY 201 LeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB 808 CTGAGCTCGCCCTCAACAAAGACTTCAACAGGAGAGTGT 849

RESULT 3
US-10-981-300-17
; Sequence 17, Application US/10981300
; Publication No. US2006009359A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; PRIOR FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 642
; TYPE: DNA
; ORGANISM: homo sapien
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US-10-981-300-17

Alignment Scores:

Pred. No.:	3,41e-87	Length:	642
Score:	937.00	Matches:	177
Percent Similarity:	91.6%	Conservative:	19
Best Local Similarity:	82.7%	Mismatches:	18
Query Match:	84.0%	Indels:	0
DB:	6	Gaps:	0

US-10-635-908-15 (1-214) x US-10-981-300-17 (1-642)

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QY 1 Aspllevalmethrnglnserglnargphnemseththryvalglyaspargvalser 20
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DB 1 GACATCCAGATGACCCAGTCTCCATCCCTCTCTGCACTCTGTAGAGACAGATCACC 60
    |||||
QY 21 IletHrCyslysa1aserGlnaenVal1aserAlaVal1atPrtyrGlnGlnlyPro 40
    |||||
DB 61 ATCATTGCGCGGCGAGTCAAGCCATTCAGCAATTATTACCTGTATCAGCAAGAACCA 120
    |||||
QY 41 GlyGlnSerProlyseu1eul1etYrSerAlaSerAsnArgTyRthrglyVal1Proasp 60
    |||||
DB 121 GGGAAAGTTCCTAAGCTCCGATCTATGCTGATCCATTCCTGCAATCAGGGGATCTCT 180
    |||||
QY 61 ArgPheThrglyserGlyserGlyThrAspPheThrLeuThrl1eserAsnMetGlnSer 80
    |||||
DB 181 CGGTTACGTGCGAGTGGATCTGGACAGATTTCACCTCCACATCAGCAGCCGCGACCT 240
    |||||
QY 81 GluAspLeuAlaaspPhePheCysGlnGlnTyRserAsnTyRProTrpThrPheGlyGly 100
    |||||
DB 241 GAAGATTGTCAACTTATTACTGTCAAAAGATGACAGTCCCGGTGAGCTTCGGCCAA 300
    |||||
QY 101 GlyThryleuGln1lelysaArgThVal1Ala1aproSerVal1Phe1lePhePro 120
    |||||
DB 301 GGGACCAAGGTGAAACCAACGACGTGGCTGACCATCTGCTTCACTTCCGCCCA 360
    |||||
QY 121 SerAspGlnGlnleu1yserGlyThrl1aserVal1Cysleu1euanAsnPhetYr 140
    |||||
DB 361 TCTGATGACGAGTTGAATCTGAACTGCTCTGTGTGGCTGCGGAAATACCTTAT 420
    |||||
QY 141 ProArgGln1AlayVal1GlnTrpLyVal1AspAsnAla1eugInserGlyAsnSerGln 160
    |||||
DB 421 CCCAGAGAGGCCAAAGTACAGTGGAGGTGATTAACCTCCCAATGGGGTAACTCCAG 480
    |||||
QY 161 GluSerVal1Thrgln1naSpSerLyAspSerThrTyRserLeuSerSerThrLeuThr 180
    |||||
DB 481 GAGAGTGTCAAGAGCAGGACAGCAAGACGACCTACAGCCTCAGACGACCTGACG 540
    |||||
QY 181 LeuSerLySa1aaspTyRglnLyGln1lyVal1AlaCysGlnVal1Thrl1eGlnGly 200
    |||||
DB 541 CTGAGCAAGACGACTACGAGAAACCAAACTTACCCCTCGGAAGTCAACCACTCAGGCG 600
    |||||
QY 201 LeuSerSerProVal1ThrylYserPheAsnArgGlyGlnCys 214
    |||||
DB 601 CTGAGCTCGCCGCTCACAAAGAGCTTCAACAGGGGAGGTGT 642
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RESULT 4

US-11-211-917-23

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/ Sequence 23, Application US/11211917
/ Publication No. US20060093600A1
/ GENERAL INFORMATION:
/ APPLICANT: BEDIAN, VAHE
/ APPLICANT: GLADUE, RONALD P.
/ APPLICANT: CORVALAN, JOSE
/ APPLICANT: JIA, XIAO-CHI
/ TITLE OF INVENTION: ANTIBODIES TO CD40
/ FILE REFERENCE: ABX-PF/3 US
/ CURRENT APPLICATION NUMBER: US/11/211,917
/ PRIOR FILING DATE: 2005-08-25
/ PRIOR APPLICATION NUMBER: US/10/292,088
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: 60/348,980
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PRIOR FILING DATE: 2001-11-09

/ NUMBER OF SEQ ID NOS: 147

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 23

/ LENGTH: 705

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-11-211-917-23

Alignment Scores:

Pred. No.:	4,84e-87	Length:	705
Score:	936.00	Matches:	179
Percent Similarity:	91.6%	Conservative:	17
Best Local Similarity:	83.6%	Mismatches:	18
Query Match:	83.9%	Indels:	0
DB:	7	Gaps:	0

US-10-635-908-15 (1-214) x US-11-211-917-23 (1-705)

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QY 1 Aspllevalmethrnglnserglnargphnemseththryvalglyaspargvalser 20
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DB 61 GACATCCAGATGACCCAGTCTCCATCCCTCTCTGCACTCTGTAGAGACAGATCACC 120
    |||||
QY 21 IletHrCyslysa1aserGlnaenVal1aserAlaVal1atPrtyrGlnGlnlyPro 40
    |||||
DB 121 ATCATTGCGCGGCGAGTCAAGCCATTCAGCAATTATTACCTGTATCAGCAAGAACCA 180
    |||||
QY 41 GlyGlnSerProlyseu1eul1etYrSerAlaSerAsnArgTyRthrglyVal1Proasp 60
    |||||
DB 181 GGGAAAGTTCCTAAGCTCCGATCTATGCTGATCCATTCCTGCAATCAGGGGATCTCT 240
    |||||
QY 61 ArgPheThrglyserGlyserGlyThrAspPheThrLeuThrl1eserAsnMetGlnSer 80
    |||||
DB 241 AGGTTACGTGCGAGTGGATCTGGACAGATTTCACCTCCACATCAGCAGCCGCGACCT 300
    |||||
QY 81 GluAspLeuAlaaspPhePheCysGlnGlnTyRserAsnTyRProTrpThrPheGlyGly 100
    |||||
DB 301 GAAGATTGTCAACTTATTACTGTCAAAAGATGACAGTCCCGGTGAGCTTCGGCCAA 360
    |||||
QY 101 GlyThryleuGln1lelysaArgThVal1Ala1aproSerVal1Phe1lePhePro 120
    |||||
DB 361 GGGACCAAGGTGAGATCAACGACGTGGCTGACCATCTGCTTCACTTCCGCCCA 420
    |||||
QY 121 SerAspGlnGlnleu1yserGlyThrl1aserVal1Cysleu1euanAsnPhetYr 140
    |||||
DB 421 TCTGATGACGAGTTGAATCTGAACTGCTCTGTGTGGCTGCGGAAATACCTTAT 480
    |||||
QY 141 ProArgGln1AlayVal1GlnTrpLyVal1AspAsnAla1eugInserGlyAsnSerGln 160
    |||||
DB 481 CCCAGAGAGGCCAAAGTACAGTGGAGGTGATTAACCTCCCAATGGGGTAACTCCAG 540
    |||||
QY 161 GluSerVal1Thrgln1naSpSerLyAspSerThrTyRserLeuSerSerThrLeuThr 180
    |||||
DB 541 GAGAGTGTCAAGAGCAGGACAGCAAGACGACCTACAGCCTCAGACGACCTGACG 600
    |||||
QY 181 LeuSerLySa1aaspTyRglnLyGln1lyVal1AlaCysGlnVal1Thrl1eGlnGly 200
    |||||
DB 601 CTGAGCAAGACGACTACGAGAAACCAAACTTACCCCTCGGAAGTCAACCACTCAGGCG 660
    |||||
QY 201 LeuSerSerProVal1ThrylYserPheAsnArgGlyGlnCys 214
    |||||
DB 661 CTGAGCTCGCCGCTCACAAAGAGCTTCAACAGGGGAGGTGT 702
    |||||
```

RESULT 5

US-10-546-594-131

```
/ Sequence 131, Application US/10546594
/ Publication No. US20060086538A1
/ GENERAL INFORMATION:
/ APPLICANT: HOSOKAWA, Saiko
/ APPLICANT: AOKI, Masahiko
/ APPLICANT: HIRAKAWA, Yoko
/ APPLICANT: ITAMI, Seima
/ APPLICANT: UMEKI, Hiroe
```



```
Db 301 GAAGTTTGGCAACTTACTATTGTCACAGCGCTACATTTTCGGCTCACTTCGGCGCA 360
Qy 101 G1YThrIysLeuGluIleYsErG1YThrAlaAlaProSerValPheIlePheProPro 120
Db 361 GGGACCAAGGCGAATCAAGAACTGTGGCTGACCATCTGTCTTCACTCTTCCGCGCA 420
Qy 121 SerAspGluGlnLeuIysSerG1YThrAlaSerValValCyLeuLeuAsnAsnPheTyr 140
Db 421 TCTGATGAGCAGATTGAAATCTGGAATGCTCTCTGTGGTGTGCTCTCTGAATTAATCTTAT 480
Qy 141 ProArgGluAlaIysValG1nTrpIysValAspAsnAlaLeuGlnSerG1YAsnSerGln 160
Db 481 CCCAGAGGCGCCAAAGTACAGAGGAAAGGTGATTAACGCCCTTCAATCCGGTAATCTCCAG 540
Qy 161 GluSerValThnGluInAspSerIysAspSerThrIYrSerLeuSerSerThrLeuThr 180
Db 541 GAGAGTGTCAAGACAGACAGACAGACAGACACCTACAGCCTCAGCAGACACCTGACG 600
Qy 181 LeuSerIysAlaAspTyrGluIysHisIysValIYrAlaCyLeuIvalThrHisGlnGly 200
Db 601 CTGACCAAGCAGACTACAGAAACAAAGCTACGCGCTGGAAGTCAACCATCAGGAGC 660
Qy 201 LeuSerSerProValThrIysSerPheAsnArgGlyGluCys 214
Db 661 CTGAGCTGCGCCGTCAACAAAGAGCTTCAACAGGAGGAGAGTGT 702
```

RESULT 9

```
US-11-211-917-87
; Sequence 87, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VARE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-87
```

Alignment Scores:

```
Pred. No.: 1.76e-83 Length: 705
Score: 901.00 Matches: 173
Percent Similarity: 91.6% Conservative: 24
Best Local Similarity: 80.5% Mismatches: 16
Query Match: 80.7% Indels: 2
DB: 7 Gaps: 2
```

US-10-635-908-15 (1-214) x US-11-211-917-87 (1-705)

```
Qy 1 AspIleValMetThrGlnSerGlnArgPheMetSerThrThrValGlyAspArgValSer 20
Db 61 GAATTTGTGTGACGACGTCTCCAGGACCCGTGTCTTGTCTCCAGGGGAAAGAGCCACC 120
Qy 21 IletnCyValAlaSerGlnAsnValIleSerAla---ValAlaTrpTyrGlnGlnIys 39
Db 121 CTCCTCGCAGGCGCCAGTACAGAGTGTACACAGCACTTACTTGGCCGTGTAACAGAGAAA 180
Qy 40 ProGlyGlnSerProIysLeuLeuIleTyrSerAlaSerAsnArgTyrThrGlyValPro 59
```

```
Db 181 CTGGCCAGGCTCCAGGCTCTCTCATATGCTGATCCAGACAGGCGCACTGGATCCCA 240
Qy 60 AspArgPheThrGlySerGlySerG1YThrAspPheThrLeuThrIleSerAsnMetGln 79
Db 241 GACAGTTCACTGACAGAGGCTCTGGGACACATTCATCTTCACCATCAGAGACTGGAG 300
Qy 80 SerGluAspLeuAlaAspPhePheCysGlnGlnIYrSerAsnTyrProTyrThrPheGly 99
Db 301 CCTGAAGATTTGGCAGTGTATTAATCTGTCAGCAGTATGACTTA---TTCACTTCCGGC 357
Qy 100 GlyGlyThrIysLeuGluIleYsErG1YThrAlaAlaProSerValPheIlePhePro 119
Db 358 CCGGACCAAGAGTGAATATCAAGAACTGTGGCTGACCATCTGTCTTCACTTCCCG 417
Qy 120 ProSerAspGluGlnLeuIysSerG1YThrAlaSerValValCyLeuLeuAsnAsnPhe 139
Db 418 CCATCTGATGAGCAGATTGAAATCTGGAATGCTCTCTGTGGTGTGCTCTGAATTAATCTTC 477
Qy 140 TyrProArgGluAlaIysValG1nTrpIysValAspAsnAlaLeuGlnSerG1YAsnSer 159
Db 478 TATCCCAAGAGGCGCCAAAGTACAGAGGAAAGGTGATTAACGCCCTTCAATCCGGTAATCTCC 537
Qy 160 GlnGluSerValThnGluInAspSerIysAspSerThrIYrSerLeuSerSerThrLeu 179
Db 538 CAGAGAGTGTCAAGACAGACAGACAGACAGACACCTACAGCCTCAGCAGACACCTG 597
Qy 180 ThrLeuSerIysAlaAspTyrGluIysHisIysValIYrAlaCyLeuIvalThrHisGln 199
Db 598 ACGCTGACCAAGCAGACTACAGAAACAAAGCTACGCGCTGGAAGTCAACCATCAG 657
Qy 200 GlyLeuSerSerProValThrIysSerPheAsnArgGlyGluCys 214
Db 658 GCGCTGAGCTGCGCCGTCAACAAAGAGCTTCAACAGGAGGAGAGTGT 702
```

RESULT 10

```
US-11-155-444-19
; Sequence 19, Application US/11155444
; Publication No. US20060104971A1
; GENERAL INFORMATION:
; APPLICANT: GARBER, ELLEN
; APPLICANT: BAILLY, VERONIQUE
; APPLICANT: BROWNING, JEFFREY L.
; TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
; FILE REFERENCE: BGNA168CN
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/US03/041393
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: 60/435,154
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/435,185
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CBB11 chimeric light
; OTHER INFORMATION: chain antibody construct
; NAME/KEY: CDS
; LOCATION: (1)..(642)
US-11-155-444-19
```

Alignment Scores:

```
Pred. No.: 1.99e-83 Length: 645
Score: 900.00 Matches: 170
Percent Similarity: 89.3% Conservative: 21
Best Local Similarity: 79.4% Mismatches: 23
Query Match: 80.6% Indels: 0
```


; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-39

Alignment Scores:

Pred. No.:	1,43e-80	Length:	720
Score:	872.50	Matches:	169
Percent Similarity:	86.8%	Conservative:	21
Best Local Similarity:	77.2%	Mismatches:	24
Query Match:	78.2%	Indels:	5
DB:	7	Gaps:	1

US-10-635-908-15 (1-214) x US-11-211-917-39 (1-720)

```
QY      1 AapllEValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB      61 GATATTGGATGATCACTCAGTCTCCACTCTCCCGCCGTCACCCCTGGAGAGCGCGCTCC 120
QY      21 lIethrCyAlaValAspSerGlnAsnValVal-----SerAlaValAlaLTP 35
DB      121 ATCTCTGCAAGCTCTAGTCAAGAGTCTTCTGTATAGTATGATGATACACTATTGGATTGG 180
QY      36 TrrGlnGlnLysProGlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyR 55
DB      181 TACCTGCAGAGGCAAGGAGGAGTCTCCACAGCTCTGATCATTTGGGTTCTAATCGGGCC 240
QY      56 ThrGlyValProAspArgPheThrGlySerGlySerGlyThyAspPheThrLeuThrIle 75
DB      241 TCCGGGGTCCCTGACAGGTTCACTGAGTCAAGTCAAGATTTTACACTGAAATTC 300
QY      76 SerAsnMetGlnSerGlnAspLeuAlaAspPhePheCysGlnGlnTySerAsnTyRPro 95
DB      301 AGCAGAGTGAAGGCTGAGATGTTGGGGTTTATTACTGATGCAAGTTTACAAACTCCA 360
QY      96 TrpThrPheGlyGlyGlyThyLysLeuGlnIleLysArgThyValAlaAlaProSerVal 115
DB      361 TTCACCTTGGCCCTGGACCAAGTGAATATCAAGAACTGTGGCTGCACCATCTGTC 420
QY      116 PheIlePheProProSerAspGlnGlnLeuLysSerGlyThyAlaSerValValCysLeu 135
DB      421 TTCATCTTCCCGCATCTATAGAGAGTGAATCTGGAATCGGCTCTGTGTGTCCTG 480
QY      136 LeuAsnAsnPheTyProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGln 155
DB      481 CTGAATTAACCTTCTATCCCAAGAGGCCCAAGTACAGTGAAGGTGATTAACGCTCCAA 540
QY      156 SerGlyAsnSerGlnLysSerValThrGlnAspSerLysAspSerThrTyRSerLeu 175
DB      541 TCGGTAACCTCCCAAGAGAGTGTCAAGAGCAGAGACAGCAAGCACTACACCTC 600
QY      176 SerSerThrLeuThrLeuSerLysAlaAspTyGlnLysIleValTyraIaCysGln 195
DB      601 AGCAGACCCCTGACGCTGACCAAGACAGACTACGAGAAACACAAAGTTACGCTCGGAA 660
QY      196 ValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB      661 GTCAACCATCAAGGCTGAGCTGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 717
```

RESULT 13

US-11-211-917-31
; Sequence 31, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: PENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40

; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-31

Alignment Scores:

Pred. No.:	2,88e-80	Length:	720
Score:	869.50	Matches:	169
Percent Similarity:	86.3%	Conservative:	20
Best Local Similarity:	77.2%	Mismatches:	25
Query Match:	77.9%	Indels:	5
DB:	7	Gaps:	1

US-10-635-908-15 (1-214) x US-11-211-917-31 (1-720)

```
QY      1 AapllEValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB      61 GATATTGGATGATCACTCAGTCTCCACTCTCCCGTCACCCCTGGAGAGCGCGCTCC 120
QY      21 lIethrCyAlaValAspSerGlnAsnValVal-----SerAlaValAlaLTP 35
DB      121 ATCTCTGCAAGCTCTAGTCAAGAGCTCTCACTACATGATGATGATACACTATTGGATTGG 180
QY      36 TrrGlnGlnLysProGlyGlnSerProLysLeuLeuIleTySerAlaSerAsnArgTyR 55
DB      181 TACCTGCAGAACCAAGGAGGAGTCTCCACACTCTGATCATTTGGGTTCTAATCGGGCC 240
QY      56 ThrGlyValProAspArgPheThrGlySerGlySerGlyThyAspPheThrLeuThrIle 75
DB      241 TCCGGGGTCCCTGACAGGTTCACTGAGTCAAGTCAAGATTTTACACTGAAATTC 300
QY      76 SerAsnMetGlnSerGlnAspLeuAlaAspPhePheCysGlnGlnTySerAsnTyRPro 95
DB      301 AGCAGAGTGAAGGCTGAGATGTTGGGGTTTATTACTGATGCAAGCTTACAAACTCCG 360
QY      96 TrpThrPheGlyGlyGlyThyLysLeuGlnIleLysArgThyValAlaAlaProSerVal 115
DB      361 TACAGTTTGGCCCAAGGAGTGAATCAAGAACTGTGGCTGCACCATCTGTC 420
QY      116 PheIlePheProProSerAspGlnGlnLeuLysSerGlyThyAlaSerValValCysLeu 135
DB      421 TTCATCTTCCCGCATCTATAGAGAGTGAATCTGGAATCGGCTCTGTGTGTCCTG 480
QY      136 LeuAsnAsnPheTyProArgGlnAlaLysValGlnTrpLysValAspAsnAlaLeuGln 155
DB      481 CTGAATTAACCTTCTATCCCAAGAGGCCCAAGTACAGTGAAGGTGATTAACGCTCCAA 540
QY      156 SerGlyAsnSerGlnLysSerValThrGlnAspSerLysAspSerThrTyRSerLeu 175
DB      541 TCGGTAACCTCCCAAGAGAGTGTCAAGAGCAGAGACAGCAAGCACTACACCTC 600
QY      176 SerSerThrLeuThrLeuSerLysAlaAspTyGlnLysIleValTyraIaCysGln 195
DB      601 AGCAGACCCCTGACGCTGACCAAGACAGACTACGAGAAACACAAAGTTACGCTCGGAA 660
QY      196 ValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
DB      661 GTCAACCATCAAGGCTGAGCTGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 717
```

RESULT 14

US-11-293-697-1838
; Sequence 1838, Application US/11293697
; Publication No. US20060105376A1

```
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/11/293,697
/ PRIOR FILING DATE: 2005-12-05
/ PRIOR APPLICATION NUMBER: US/10/108,260
/ PRIOR FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1838
/ LENGTH: 929
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-293-697-1838

Alignment Scores:
Pred. No.: 5,61e-80 Length: 929
Score: 868.00 Matches: 166
Percent Similarity: 86.9% Conservative: 20
Best Local Similarity: 77.6% Mismatches: 28
Query Match: 77.8% Indels: 0
DB: Gaps: 0

US-10-635-908-15 (1-214) x US-11-293-697-1838 (1-929)

QY 1 AsptleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 91 GACACTCAGATGACCCAGCTCCGACCTCCCTGTCGATCTGGAGGACAGATCACC 150
QY 21 IleThrCysAlaSerGlnAsnValValSerAlaValAlaTrpTyrglnGlnLeu 40
DB 151 ATACATTCGACAGCGACGTCACGACATGTAAGATTTTAAACGGTATCGTACAAACA 210
QY 41 GlyGlnSerProIlySleuLeuIleTySerAlaSerAsnArgTyThrGlyValProAsp 60
DB 211 GGCAGAGCCCTAAGCCCTCATCCACGATGCTCCAGATCAGAAAAGAGTCCACGA 270
QY 61 ArgPheThrGlySerGlySerGlyThrAspPheThrIleSerAsnMetGlnSer 80
DB 271 AGATTCAAGTGAAGTGAATTGGACAGATTTTAACTTTTTCACAAACCTACAACT 330
QY 81 GluAspLeuAlaAspPhePheCysGlnGlnTySerAsnTyProTrpThrPheGly 100
DB 331 GAAGATCTTCGACATTAATTAATCAAAATTGGTCTCTGCTCGACCTTGGCCAG 390
QY 101 GlyThrIlySleuGlnIleTyArgThrValAlaAlaProSerValPheIlePhePro 120
DB 391 GGGACCAAGCTTCAGATCAATCGAAGCTGGCTGCACCATCTGTCTTCATCTCCGCA 450
QY 121 SerAspGlnGlnLeuIlySerGlyThrAlaSerValValCysLeuLeuAsnPheTy 140
DB 451 TCTGATAGCAGGTTGAATCTGGAATCTGCTGTGTGTGCTGTGTAATTAATCTTAT 510
QY 141 ProArgGlnAlaIlyValGlnTrpIlyValAspAsnAlaLeuGlnSerGlyAsnSerGln 160
DB 511 CCCAGAGAGCCCAAGTACACTGAGAGGTGATTAACCCCTCCATAGGGTAACTCCAG 570
QY 161 GluSerValThrGlnIlyAspSerIlyAspSerThrTySerLeuSerSerThrLeuThr 180
DB 571 GAGAGTGTCAAGAGCAGACAGACAGACAGACCTACAGCTCAGAGCAGACCTGAG 630
QY 181 LeuSerIlyAlaAspTyArgIlyIlyValIlyValIlyValIlyValIlyValIly 200
DB 631 CTGAGCAAGGAGCTACGAGAAACACAAAGTCTACGGCTGAGAGTCAACCATCAAGGC 690
QY 201 LeuSerSerProValThrIlySerPheAsnArgGlyGluCys 214
DB 691 CTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 732

RESULT 15
US-11-211-917-15
/ Sequence 15, Application US/11211917
```

```
/ Publication No. US20060093600A1
/ GENERAL INFORMATION:
/ APPLICANT: BEDIAN, VARE
/ APPLICANT: GLADUE, RONALD P.
/ APPLICANT: CORVALAN, JOSE
/ APPLICANT: JIA, XIAO-CHI
/ APPLICANT: FENG, XIAO
/ TITLE OF INVENTION: ANTIBODIES TO CD40
/ FILE REFERENCE: ABX-PF/3 US
/ CURRENT APPLICATION NUMBER: US/11/211,917
/ PRIOR FILING DATE: 2005-08-25
/ PRIOR APPLICATION NUMBER: US/10/292,088
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: 60/348,980
/ PRIOR FILING DATE: 2001-11-09
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 15
/ LENGTH: 720
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-211-917-15

Alignment Scores:
Pred. No.: 4.6e-80 Length: 720
Score: 867.50 Matches: 169
Percent Similarity: 86.3% Conservative: 20
Best Local Similarity: 77.2% Mismatches: 25
Query Match: 77.7% Indels: 5
DB: Gaps: 1

US-10-635-908-15 (1-214) x US-11-211-917-15 (1-720)

QY 1 AsptleValMetThrGlnSerGlnArgPheMetSerThrThyValGlyAspArgValSer 20
DB 61 GATATTGTATGATGATCACTGCTCCCTCCGCTACCTCCGAGAGCCGCTCC 120
QY 21 IleThrCysAlaSerGlnAsnValVal-----SerAlaValAlaTrp 35
DB 121 ATCTCTGACAGGCTAGTACAGACCTCTGTATAGTATGATGATACAACTTTTGATGG 180
QY 36 TyrGlnGlnIlySerProIlyGlnSerProIlySleuLeuIleTySerAlaSerAsnArgTy 55
DB 181 TACCTCAGAGAGCAGGAGCTCCACACCTCTGATCTAATTTGGCTTAAATCGGCC 240
QY 56 ThrGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrIle 75
DB 241 TCCGGGGTCCCTTACAGATTCAGTGCAGAGATCAGGACAGATTTTACACGAAATC 300
QY 76 SerAsnMetGlnSerGlnAspLeuAlaAspPheCysGlnGlnTySerAsnTyPro 95
DB 301 AGCAGAGTGAAGGCTGAGATGTTGGGGTTATTATTCGATGACAGCTTCAAACTCT 360
QY 96 TrpThrPheGlyGlyGlyThrIlySleuGlnIleTyArgThrValAlaAlaProSerVal 115
DB 361 CGGACGTTCCGCAAGGAGCAAGGTGAATCAAGAACTGTGGCTGCACATCTGTC 420
QY 116 PheIlePheProPheSerAspGlnGlnLeuIlySerGlyThrAlaSerValValCysLeu 135
DB 421 TTCACTTCCCGCATGTATGACAGCTTGAATCTGGAATCTGCTGTGTGTGCTG 480
QY 136 LeuAsnAsnPheTyProArgGlnAlaIlyValGlnTrpIlyValAspAsnAlaLeuGln 155
DB 481 CTGAATAACTTCTATCCCAAGAGGCCAAAGTACAGAGGAGGATTAACGCTCCAA 540
QY 156 SerGlyAsnSerGlnGlnIlySerValThrGlnIlyAspSerIlyAspSerThrTySerLeu 175
DB 541 TCCGGTAACTCCCAAGGAGAGTGTACAGACAGGACAGCAAGGACACACCTTACAGCTC 600
QY 176 SerSerThrLeuThrLeuSerIlyAlaAspTyArgIlyIlyValIlyValIlyValIly 195
DB 601 AGCAGACCTCTGAGCTGAGCAAAAGCAGACTAGAGAAACAAAGTCTAGCTGCGAA 660
```

Oy 196 ValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGlyCys 214
 |||||
 Db 661 GTCACCCATCAGGGCCTGAGCTGCGCCGTCACAAAGAGCTCAACAGGGAGAGTGT 717
 |||||

Search completed: June 3, 2006, 09:17:10
 Job time : 28.4204 secs